

1

SEQUENCE LISTING

<110> SunGene GmbH & Co.KGaA

<120> Transgenic expression cassettes for expressing nucleic acids
in the flower of plants

<130> AE20020666

<140>

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<160> 83

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Tagetes erecta

<220>

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<222> (1)..(312)

<400> 1

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aattaaaata aagagaagag aaagattaag aggggtgatgg ggatattaaa gacggscaat 180
atagtgatgc cacgtagaaa aaggtaagtg aaaacataca acgtggcttt aaaagatggc 240
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<221> misc_feature

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atagtgatgc cacgtagaaa aaggtaagtg aaaacataca acgtggcttt aaaagatggc 240
ttggctgcta atcaactcaa ctcaactcat atcctatcca ttcaaattca attcaattct 300
attgaatgca aagcaaagca aaggttgttt gttgttggtg ttgagagaca ctccaatcca 360
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<221> promoter

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<220>

<221> sig_peptide

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<221> CDS

<222> (445)..(537)

<223> coding for transit peptide of epsilon cyclase

<400> 3

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 aattaaaata aagagaagag aaagattaag aggggtgatgg ggatattaaa gacggscaat 180
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 attgaatgca aagcaaagca aagggttgtt gttgttggtg ttgagagaca ctccaatcca 360
 aacagatata aggcgtgact ggatatttct ctctcgttcc taacaacagc aacgaagaag 420
 aaaaagaatc attactaaca atca atg agt atg aga gct gga cac atg acg 471

Met Ser Met Arg Ala Gly His Met Thr

1

5

gca aca atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga 519
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<213> Tagetes erecta

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Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys
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<213> Tagetes erecta

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<221> misc_feature

<222> (1)..(6)

<223> restriction site

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<222> (451)..(456)

<223> restriction site

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 <222> (7)..(450)
 <223> coding for promoter and 5'-UTR region

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 atatagtgat gccacgtaga aaaaggtaag tgaaaacata caacgtggct ttaaaagatg 240
 gcttggctgc taatcaactc aactcaactc atatcctatc cattcaaatt caattcaatt 300
 ctattgaatg caaagcaaag caaaggttgt ttgttgttgt tgttgagaga cactccaatc 360
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 <222> (1)..(6)
 <223> restriction site

<220>
 <221> misc_feature
 <222> (538)..(543)
 <223> restriction site

<220>
 <221> misc_feature
 <222> (7)..(542)
 <223> coding for promoter - 5'-UTR - signal peptide region

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 caaacagata caaggcgtga ctggatattt ctctctcgtt cctaacaaca gcaacgaaga 420
 agaaaaagaa tcattactaa caatcaatga gtatgagagc tggacacatg acggcaacaa 480
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 tgg 543

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 <213> *Arabidopsis thaliana*

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 gctgcgtatt ctactacaa tgtggccaca cagacctcgt ttcttcagct gatgaatgat 180
 ggcgctaattg tctcaaagca aaagggtttc gatgtgttca acgcgttgga tgtgatgcac 240
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 ctctacaatt accgtttgaa aagtgccttg aagccagcgg aactcgggct tgttctctta 360
 taagctcaac aacttgattt gatggtatca acaaacttga aatttgtctc tctttttttt 420
 tcttcagtct gaactacttc tcccatggtt tactgaaact gagtttaatt attttggcaa 480

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tgcaattttg gatttttgctt ttagtttcac ttgtgttctc tgagagagtt gaccctgaga 540
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<210> 8

<211> 1169

<212> DNA

<213> *Oryza sativa*

<400> 8

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tcgtcgcggt cgggtgggtgc cgggcggagc ggttttttag ggaggggtcg gcggccggcg 240
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ggacgacgac gaggaagggt ggagagagga atcaactacc gacgacagcg gaggcggcg 360
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cctccgttcc accgcgagcc cgcgcgcgctc cgttcgagc gctcgccgt cgccgctccg 480
ctgctgtgca gtcccgcgc cgcgctcgcc ctgactgaag aagaaaagag agaagagaga 540
aaagagaagg gaaggagaag aaaatagaag aaaaaaatat gtgcagctga tgtatgagcc 600
ccacatactc ttttttaatc ttttttgctg actacgatgc cagtcagcg aaaccaccta 660
tatatactac cataggatct tgagtgcacg gtttatatga gtttaggagt atacattttt 720
agttttatgg ttaagggatc ataaaaaatt ctcgctatta agttgagtga cgcgcagtg 780
acttattact caaacttaac agcgtttgat ccattcacat ccggcccata gcagcccata 840
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accgctccc tctcctctc cctcctcta caatggccgc agcagcagca gccagcagca 1080
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<210> 9

<211> 1830

<212> DNA

<213> *Tagetes erecta*

<220>

<221> CDS

<222> (141)..(1688)

<223> coding for epsilon-cyclase

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agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173
Met Ser Met Arg Ala Gly His Met Thr Ala Thr
1 5 10
atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221
Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr
15 20 25
aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa 269
Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln
30 35 40

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gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tcg gag ctg	317
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Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser	
60 65 70 75	
cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt	413
Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser	
80 85 90	
aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt	461
Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu	
95 100 105	
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Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile	
110 115 120	
ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa	557
Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu	
125 130 135	
ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat	605
Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp	
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Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala	
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Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg	
175 180 185	
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Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile	
190 195 200	
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Thr Glu Ala Pro Asn Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile	
205 210 215	
aca att cca tgc agg ctt gct act gtc gct tct gga gca gct tct gga	845
Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly	
220 225 230 235	
aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca	893
Lys Leu Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr	
240 245 250	
gct tat ggt ata gag gtt gag gtt gaa agc ata ccc tat gat cca agc	941
Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser	
255 260 265	
cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa	989
Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln	
270 275 280	
tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct	1037
Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser	
285 290 295	
cca act aaa gta ttc ttt gag gaa act tgt ttg gct tca aaa gag gcc	1085
Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala	
300 305 310 315	

atg cct ttt gag tta ttg aag aca aaa ctc atg tca aga tta aag act 1133
 Met Pro Phe Glu Leu Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr
 320 325 330

atg ggg atc cga ata acc aaa act tat gaa gag gaa tgg tca tat att 1181
 Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile
 335 340 345

cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt 1229
 Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe
 350 355 360

ggt gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta 1277
 Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val
 365 370 375

aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att 1325
 Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile
 380 385 390 395

tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca 1373
 Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr
 400 405 410

acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg 1421
 Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg
 415 420 425

aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag 1469
 Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln
 430 435 440

atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg 1517
 Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu
 445 450 455

ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act 1565
 Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr
 460 465 470 475

gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc 1613
 Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser
 480 485 490

ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga 1661
 Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly
 495 500 505

aca atg tta aaa gcg tat ctc acg ata taaataactc tagtcgcat 1708
 Thr Met Leu Lys Ala Tyr Leu Thr Ile
 510 515

cagtttagat tataggcaca tcttgcatat atatattgtat aaaccttatg tgtgctgtat 1768
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<210> 10
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 <212> PRT
 <213> Tagetes erecta
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Gln	Gln	Asn	Lys	Ser	Met	Asp	Ala	Gln	Ser	Ser	Leu	Ser	Gln	Lys	Leu		
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Pro	Arg	Val	Pro	Ile	Gly	Gly	Gly	Gly	Asp	Ser	Asn	Cys	Ile	Leu	Asp		
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Leu	Val	Val	Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Gly	Glu		
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Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Ile	Gly	Leu	Gly		
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Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Gln	Tyr		
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Glu	Leu	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Ile	Glu		
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	385				390					395					400		
Ser	Lys	Gln	Met	Leu	Asp	His	Gly	Arg	Tyr	Thr	Thr	Asn	Ile	Ser	Lys		
				405					410					415			

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 420 425 430
 Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly
 435 440 445
 Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp
 450 455 460
 Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe
 465 470 475 480
 Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu
 485 490 495
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 500 505 510
 Tyr Leu Thr Ile
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<210> 11
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 <212> DNA
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<220>
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 Met Ser
 1
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 Met Arg Ala Gly His Met Thr Ala Thr Met Ala Ala Phe Thr Cys Pro
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 agg ttt atg act agc atc aga tac acg aag caa att aag tgc aac gct 274
 Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys Asn Ala
 20 25 30
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 Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu Glu Asp
 35 40 45 50
 tat gtg aaa gcc ggt gga tcg gag ctg ctt ttt gtt caa atg caa cag 370
 Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met Gln Gln
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 Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu Pro Arg
 70 75 80
 gta cca ata gga gga gga gga gac agt aac tgt ata ctg gat ttg gtt 466
 Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp Leu Val
 85 90 95
 gta att ggt tgt ggt cct gct ggc ctt gct ctt gct gga gaa tca gcc 514
 Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu Ser Ala
 100 105 110

aag cta ggc ttg aat gtc gca ctt atc ggc cct gat ctt cct ttt aca	562
Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro Phe Thr	
115 120 125 130	
aat aac tat ggt gtt tgg gag gat gaa ttt ata ggt ctt gga ctt gag	610
Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly Leu Glu	
135 140 145	
ggc tgt att gaa cat gtt tgg cga gat act gta gta tat ctt gat gac	658
Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu Asp Asp	
150 155 160	
aac gat ccc att ctc ata ggt cgt gcc tat gga cga gtt agt cgt gat	706
Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Asp	
165 170 175	
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Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly Val Ser	
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Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn Gly Leu	
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Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg Leu Ala	
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act gtc gct tct gga gca gct tct ggg aaa ctt ttg cag tat gaa ctt	898
Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Leu	
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Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Tyr Glu Val Glu	
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Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr	
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Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln Tyr Pro	
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aca ttt ttg tat gtc atg cca atg tct cca act aaa gta ttc ttt gag	1090
Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe Phe Glu	
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Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu Leu Lys	
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Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu	
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Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser	
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 Lys Ile Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp Leu Gly Arg
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 Tyr Thr Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu
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 Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile
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 Val Gln Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe
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 Arg Leu Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser
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 tca act gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg 1666
 Ser Thr Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro
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 His Ser Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr
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 Gly Gly Thr Met Leu Lys Ala Tyr Leu Thr Ile
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 Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
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 Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
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Ser	Ala	Lys	Leu	Gly	Leu	Asn	Val	Ala	Leu	Ile	Gly	Pro	Asp	Leu	Pro	115	120	125
Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Ile	Gly	Leu	Gly	130	135	140
Leu	Glu	Gly	Cys	Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Val	Val	Tyr	Leu	145	150	155
Asp	Asp	Asn	Asp	Pro	Ile	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	165	170	175
Arg	Asp	Leu	Leu	His	Glu	Glu	Leu	Leu	Thr	Arg	Cys	Met	Glu	Ser	Gly	180	185	190
Val	Ser	Tyr	Leu	Ser	Ser	Lys	Val	Glu	Arg	Ile	Thr	Glu	Ala	Pro	Asn	195	200	205
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Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Gln	Tyr	225	230	235
Glu	Leu	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Tyr	Glu	245	250	255
Val	Glu	Val	Glu	Ser	Ile	Pro	Tyr	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	260	265	270
Asp	Tyr	Arg	Asp	Tyr	Thr	Lys	His	Lys	Ser	Gln	Ser	Leu	Glu	Ala	Gln	275	280	285
Tyr	Pro	Thr	Phe	Leu	Tyr	Val	Met	Pro	Met	Ser	Pro	Thr	Lys	Val	Phe	290	295	300
Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Lys	Glu	Ala	Met	Pro	Phe	Glu	Leu	305	310	315
Leu	Lys	Thr	Lys	Leu	Met	Ser	Arg	Leu	Lys	Thr	Met	Gly	Ile	Arg	Ile	325	330	335
Thr	Lys	Thr	Tyr	Glu	Glu	Tyr	Leu	Val	Ala	Cys	Gln	Tyr	Leu	Glu	Glu	340	345	350
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Asn	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	370	375	380
Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Asn	Tyr	Ala	Ala	Val	385	390	395
Ile	Ala	Lys	Ile	Leu	Gly	Lys	Gly	Asn	Ser	Lys	Gln	Met	Leu	Asp	Leu	405	410	415
Gly	Arg	Tyr	Thr	Thr	Asn	Ile	Ser	Lys	Gln	Ala	Trp	Glu	Thr	Leu	Trp	420	425	430
Pro	Leu	Glu	Arg	Lys	Arg	Gln	Arg	Ala	Phe	Phe	Leu	Phe	Gly	Leu	Ala	435	440	445
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Phe	Phe	Arg	Leu	Pro	Thr	Trp	Met	Trp	Trp	Gly	Phe	Leu	Gly	Ser	Ser	465	470	475
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Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr Phe Pro Ser Trp																
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Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr Ser Tyr Arg Asn																
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Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly Gly Gly Ser Ser																
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Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe Ala Asp Glu Glu																
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Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe Val Gln Met Gln																
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Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val Asp Lys Leu Pro																
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Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp Leu Val Val Ile Gly Cys																
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Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly Leu																
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Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly																
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Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln Lys Cys Ile Glu																
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His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp Asp Lys Pro Ile																
165 170 175 180																

acc att ggc cgt gct tat gga aga gtt agt cga cgt ttg ctc cat gag	691
Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg Leu Leu His Glu	
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Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu Arg Leu Val Ala	
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Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala Thr Val Ala Ser	
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Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly Pro Arg	
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Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn Ser	
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Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys Thr Lys Leu Met	
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14

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 Met Ile Lys Thr Tyr Leu Lys Val
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 Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr
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 Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln
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 Lys Cys Ile Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp
 165 170 175
 Asp Lys Pro Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg
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 Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser
 195 200 205

15

Tyr	Leu	Ser	Ser	Lys	Val	Asp	Ser	Ile	Thr	Glu	Ala	Ser	Asp	Gly	Leu	210	215	220
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Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Gln	Tyr	Glu	Val	245	250	255
Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	260	265	270
Val	Glu	Asn	Ser	Pro	Tyr	Asp	Pro	Asp	Gln	Met	Val	Phe	Met	Asp	Tyr	275	280	285
Arg	Asp	Tyr	Thr	Asn	Glu	Lys	Val	Arg	Ser	Leu	Glu	Ala	Glu	Tyr	Pro	290	295	300
Thr	Phe	Leu	Tyr	Ala	Met	Pro	Met	Thr	Lys	Ser	Arg	Leu	Phe	Phe	Glu	305	310	315
Glu	Thr	Cys	Leu	Ala	Ser	Lys	Asp	Val	Met	Pro	Phe	Asp	Leu	Leu	Lys	325	330	335
Thr	Lys	Leu	Met	Leu	Arg	Leu	Asp	Thr	Leu	Gly	Ile	Arg	Ile	Leu	Lys	340	345	350
Thr	Tyr	Glu	Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	355	360	365
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His	Pro	Ala	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	385	390	395
Lys	Tyr	Ala	Ser	Val	Ile	Ala	Glu	Ile	Leu	Arg	Glu	Glu	Thr	Thr	Lys	405	410	415
Gln	Ile	Asn	Ser	Asn	Ile	Ser	Arg	Gln	Ala	Trp	Asp	Thr	Leu	Trp	Pro	420	425	430
Pro	Glu	Arg	Lys	Arg	Gln	Arg	Ala	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	435	440	445
Ile	Val	Gln	Phe	Asp	Thr	Glu	Gly	Ile	Arg	Ser	Phe	Phe	Arg	Thr	Phe	450	455	460
Phe	Arg	Leu	Pro	Lys	Trp	Met	Trp	Gln	Gly	Phe	Leu	Gly	Ser	Thr	Leu	465	470	475
Thr	Ser	Gly	Asp	Leu	Val	Leu	Phe	Ala	Leu	Tyr	Met	Phe	Val	Ile	Ser	485	490	495
Pro	Asn	Asn	Leu	Arg	Lys	Gly	Leu	Ile	Asn	His	Leu	Ile	Ser	Asp	Pro	500	505	510
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Ser Arg Arg Val Val Pro Arg Ala Val Glu Pro Arg Arg Arg Gly Arg	
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Trp Met Val Arg Cys Val Ala Thr Glu Lys His Lys Asp Ala Ala Ala	
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Arg Arg Gly Gly Val Glu Val Glu Phe Ala Asp Glu Glu Asp Tyr Val	
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Lys Gly Gly Gly Gly Glu Leu Leu Tyr Val Gln Met Gln Ala Ser Lys	
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Ser Met Asp Ser Gln Ser Lys Ile Ser Ser Lys Leu Leu Pro Ile Pro	
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Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu	
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Lys Asp Thr Ile Val Tyr Leu Asp Gly Asn Lys Pro Ile Met Ile Gly	
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Arg Ala Tyr Gly Arg Val His Arg Asp Leu Leu His Glu Glu Leu Leu	
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Lys Ile Met Glu Ser Pro Asp Gly His Arg Val Val Cys Cys Glu Gly	
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Asp Arg Glu Val Leu Cys Arg Leu Ala Ile Val Ala Ser Gly Ala Ala	
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Ser Gly Arg Leu Leu Glu Tyr Glu Val Gly Gly Pro Arg Val Cys Val	
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Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	Asn	Asn	Pro	Tyr	Asp	
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Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Cys	Phe	Lys	Asp	Lys	
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Phe	Ser	His	Pro	Glu	Gln	Gly	Asn	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	
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Met	Ser	Ser	Thr	Arg	Ile	Phe	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Lys	
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gat	gca	atg	gga	gtt	cat	att	cga	aaa	gta	tac	gag	gag	gaa	tgg	tcc	1104
Asp	Ala	Met	Gly	Val	His	Ile	Arg	Lys	Val	Tyr	Glu	Glu	Glu	Trp	Ser	
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tac	att	cct	gtt	gga	ggg	tcc	tta	cca	aat	aca	gac	cag	aaa	aat	ctc	1152
Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Asp	Gln	Lys	Asn	Leu	
	370					375					380					
gca	ttt	ggc	gca	gca	agt	atg	gtg	cat	cct	gca	acc	gga	tac	tcg		1200
Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	
385					390					395				400		
gtg	gtt	aga	tca	ttg	tct	gaa	gct	cca	aga	tat	gca	tct	gtg	ata	tct	1248
Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Arg	Tyr	Ala	Ser	Val	Ile	Ser	
				405					410					415		
gat	atc	ttg	aga	aac	cgt	gtc	tac	cct	gga	gaa	tat	ttg	cct	gga	acc	1296
Asp	Ile	Leu	Arg	Asn	Arg	Val	Tyr	Pro	Gly	Glu	Tyr	Leu	Pro	Gly	Thr	
			420					425					430			
tct	caa	agt	tcc	agt	cca	tca	atg	ctt	gca	tgg	aga	aca	tta	tgg	ccc	1344
Ser	Gln	Ser	Ser	Ser	Pro	Ser	Met	Leu	Ala	Trp	Arg	Thr	Leu	Trp	Pro	
		435					440					445				
caa	gaa	cgg	aaa	cgt	caa	cga	tca	ttc	ttc	ctt	ttt	ggg	ctg	gct	ttg	1392
Gln	Glu	Arg	Lys	Arg	Gln	Arg	Ser	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	
	450					455					460					
ata	atc	caa	ctg	aat	aac	gaa	ggc	att	cag	aca	ttc	ttt	gaa	acc	ttt	1440
Ile	Ile	Gln	Leu	Asn	Asn	Glu	Gly	Ile	Gln	Thr	Phe	Phe	Glu	Thr	Phe	
465					470					475					480	
ttc	cgg	ttg	ccc	aaa	tgg	atg	tgg	cga	gga	ttc	ctt	ggt	tcg	acg	ctt	1488
Phe	Arg	Leu	Pro	Lys	Trp	Met	Trp	Arg	Gly	Phe	Leu	Gly	Ser	Thr	Leu	
				485					490				495			
tct	tca	gtg	gat	ctc	ata	ctc	ttt	gca	ttc	tac	atg	ttc	aca	att	gcg	1536
Ser	Ser	Val	Asp	Leu	Ile	Leu	Phe	Ala	Phe	Tyr	Met	Phe	Thr	Ile	Ala	
			500					505					510			
ccg	aac	caa	atg	cga	atg	aac	ctt	gtc	aga	cat	ctc	ctc	tct	gat	ccg	1584
Pro	Asn	Gln	Met	Arg	Met	Asn	Leu	Val	Arg	His	Leu	Leu	Ser	Asp	Pro	
		515					520					525				
acc	ggc	tca	acg	atg	atc	aag	acc	tac	ctg	acc	ttg	taa				1623
Thr	Gly	Ser	Thr	Met	Ile	Lys	Thr	Tyr	Leu	Thr	Leu					
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<210> 16

<211> 540

<212> PRT

<213> · *Oryza sativa*

<400> 16

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Arg	Ala	Ala	Trp 20	Gly	Ala	Ala	Ala	Ala	Gly 25	Ala	Gly	Ala	Glu 30	Gly	Arg
Ser	Arg	Arg 35	Val	Val	Pro	Arg	Ala 40	Val	Glu	Pro	Arg	Arg 45	Arg	Gly	Arg
Trp	Met 50	Val	Arg	Cys	Val	Ala 55	Thr	Glu	Lys	His 60	Lys	Asp	Ala	Ala	Ala
Arg 65	Arg	Gly	Gly	Val	Glu 70	Val	Glu	Phe	Ala	Asp 75	Glu	Glu	Asp	Tyr	Val 80
Lys	Gly	Gly	Gly	Gly 85	Glu	Leu	Leu	Tyr	Val 90	Gln	Met	Gln	Ala	Ser 95	Lys
Ser	Met	Asp	Ser 100	Gln	Ser	Lys	Ile	Ser 105	Ser	Lys	Leu	Leu	Pro 110	Ile	Pro
Asp	Glu	Asn 115	Ser	Val	Leu	Asp 120	Leu	Val	Ile	Ile	Gly	Cys 125	Gly	Pro	Ala
Gly	Leu 130	Ser	Leu	Ala	Ala 135	Glu	Ser	Ala	Lys	Lys 140	Gly	Leu	Asn	Val	Gly
Leu 145	Ile	Gly	Pro	Asp	Leu 150	Pro	Phe	Thr	Asn	Asn 155	Tyr	Gly	Val	Trp	Glu 160
Asp	Glu	Phe	Lys 165	Asp	Leu	Gly	Leu	Glu	Ser 170	Cys	Ile	Glu	His	Val 175	Trp
Lys	Asp	Thr 180	Ile	Val	Tyr	Leu	Asp	Gly 185	Asn	Lys	Pro	Ile	Met 190	Ile	Gly
Arg	Ala	Tyr 195	Gly	Arg	Val	His	Arg 200	Asp	Leu	Leu	His	Glu 205	Glu	Leu	Leu
Arg	Arg 210	Cys	Tyr	Asp	Ala	Gly 215	Val	Thr	Tyr	Leu	Ser 220	Ser	Lys	Val	Asp
Lys 225	Ile	Met	Glu	Ser	Pro 230	Asp	Gly	His	Arg	Val 235	Val	Cys	Cys	Glu	Gly 240
Asp	Arg	Glu	Val 245	Leu	Cys	Arg	Leu	Ala	Ile 250	Val	Ala	Ser	Gly	Ala 255	Ala
Ser	Gly	Arg	Leu 260	Leu	Glu	Tyr	Glu	Val 265	Gly	Gly	Pro	Arg	Val 270	Cys	Val
Gln	Thr 275	Ala	Tyr	Gly	Val	Glu	Val 280	Glu	Val	Glu	Asn	Asn 285	Pro	Tyr	Asp
Pro	Ser 290	Leu	Met	Val	Phe	Met 295	Asp	Tyr	Arg	Asp	Cys 300	Phe	Lys	Asp	Lys
Phe 305	Ser	His	Pro	Glu	Gln 310	Gly	Asn	Pro	Thr	Phe 315	Leu	Tyr	Ala	Met	Pro 320
Met	Ser	Ser	Thr 325	Arg	Ile	Phe	Phe	Glu	Glu 330	Thr	Cys	Leu	Ala	Ser 335	Lys
Glu	Ala	Met	Pro 340	Phe	Asp	Leu	Leu	Lys 345	Lys	Arg	Leu	Met	Ser 350	Arg	Leu

Asp	Ala	Met	Gly	Val	His	Ile	Arg	Lys	Val	Tyr	Glu	Glu	Glu	Trp	Ser
		355					360					365			
Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Asp	Gln	Lys	Asn	Leu
	370					375					380				
Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser
385					390					395					400
Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Arg	Tyr	Ala	Ser	Val	Ile	Ser
				405					410					415	
Asp	Ile	Leu	Arg	Asn	Arg	Val	Tyr	Pro	Gly	Glu	Tyr	Leu	Pro	Gly	Thr
			420					425					430		
Ser	Gln	Ser	Ser	Ser	Pro	Ser	Met	Leu	Ala	Trp	Arg	Thr	Leu	Trp	Pro
		435					440					445			
Gln	Glu	Arg	Lys	Arg	Gln	Arg	Ser	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu
	450					455					460				
Ile	Ile	Gln	Leu	Asn	Asn	Glu	Gly	Ile	Gln	Thr	Phe	Phe	Glu	Thr	Phe
465					470					475					480
Phe	Arg	Leu	Pro	Lys	Trp	Met	Trp	Arg	Gly	Phe	Leu	Gly	Ser	Thr	Leu
				485					490					495	
Ser	Ser	Val	Asp	Leu	Ile	Leu	Phe	Ala	Phe	Tyr	Met	Phe	Thr	Ile	Ala
			500					505					510		
Pro	Asn	Gln	Met	Arg	Met	Asn	Leu	Val	Arg	His	Leu	Leu	Ser	Asp	Pro
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Thr	Gly	Ser	Thr	Met	Ile	Lys	Thr	Tyr	Leu	Thr	Leu				
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<211> 10

<212> PRT

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<223> Description of the artificial sequence: protein motif for epsilon-cyclase

<220>

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<223> G/C variation

<220>

<221> VARIANT

<222> (8)

<223> A/S variation

<220>

<221> VARIANT

<222> (9)

<223> V/L variation

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<210> 18

<211> 8

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<220>
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motif for epsilon-cyclase
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<223> L/I variation
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<222> (2)
<223> N/G/S variation
<220>
<221> VARIANT
<222> (7)
<223> K/R variation
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<222> (8)
<223> V/L variation
<400> 18
Leu Asn Arg Xaa Tyr Gly Lys Val
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<210> 19
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<223> Y/W variation
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<223> A/V variation
<220>
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<222> (8)

<223> P/A variation

<400> 20

Pro Thr Phe Leu Tyr Ala Met Pro

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5

<210> 21

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif for epsilon-cyclase

<220>

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<222> (7)

<223> S/A-variation

<220>

<221> VARIANT

<222> (11)

<223> M/S variation

<220>

<221> VARIANT

<222> (13)

<223> A/V variation

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5

10

<210> 22

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif for epsilon-cyclase

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<223> R/K variation

<400> 22

Leu Trp Pro Xaa Glu Arg Arg Arg Gln Arg Xaa Phe Phe

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<210> 23

<211> 1780

<212> DNA

<213> Lactuca sativa

<220>

<221> CDS

<222> (77)..(1675)

<223> coding for epsilon-cyclase

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Met Glu Cys Phe Gly Ala Arg Asn Met Thr Ala Thr	
1 5 10	
atg gcg gtt ttt acg tgc cct aga ttc acg gac tgt aat atc agg cac	160
Met Ala Val Phe Thr Cys Pro Arg Phe Thr Asp Cys Asn Ile Arg His	
15 20 25	
aaa ttt tcg tta ctg aaa caa cga aga ttt act aat tta tca gca tcg	208
Lys Phe Ser Leu Leu Lys Gln Arg Arg Phe Thr Asn Leu Ser Ala Ser	
30 35 40	
tct tcg ttg cgt caa att aag tgc agc gct aaa agc gac cgt tgt gta	256
Ser Ser Leu Arg Gln Ile Lys Cys Ser Ala Lys Ser Asp Arg Cys Val	
45 50 55 60	
gtg gat aaa caa ggg att tcc gta gca gac gaa gaa gat tat gtg aag	304
Val Asp Lys Gln Ile Ser Val Ala Asp Glu Glu Asp Tyr Val Lys	
65 70 75	
gcc ggt gga tcg gag ctg ttt ttt gtt caa atg cag cgg act aag tcc	352
Ala Gly Gly Ser Glu Leu Phe Phe Val Gln Met Gln Arg Thr Lys Ser	
80 85 90	
atg gaa agc cag tct aaa ctt tcc gaa aag cta gca cag ata cca att	400
Met Glu Ser Gln Ser Lys Leu Ser Glu Lys Leu Ala Gln Ile Pro Ile	
95 100 105	
gga aat tgc ata ctt gat ctg gtt gta atc ggt tgt ggc cct gct ggc	448
Gly Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly	
110 115 120	
ctt gct ctt gct gca gag tca gcc aaa cta ggg ttg aac gtt gga ctc	496
Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly Leu Asn Val Gly Leu	
125 130 135 140	
att ggc cct gat ctt cct ttt aca aac aat tat ggt gtt tgg cag gat	544
Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Gln Asp	
145 150 155	
gaa ttt ata ggt ctt gga ctt gaa gga tgc att gaa cat tct tgg aaa	592
Glu Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Ser Trp Lys	
160 165 170	
gat act ctt gta tac ctt gat gat gct gat ccc atc cgc ata ggt cgt	640
Asp Thr Leu Val Tyr Leu Asp Asp Ala Asp Pro Ile Arg Ile Gly Arg	
175 180 185	
gca tat ggc aga gtt cat cgt gat tta ctt cat gaa gag ttg tta aga	688
Ala Tyr Gly Arg Val His Arg Asp Leu Leu His Glu Glu Leu Leu Arg	
190 195 200	
agg tgt gtg gaa tca ggt gtt tca tat cta agc tcc aaa gta gaa aga	736
Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg	
205 210 215 220	
atc act gaa gct cca aat ggc tat agt ctc att gaa tgt gaa ggc aat	784
Ile Thr Glu Ala Pro Asn Gly Tyr Ser Leu Ile Glu Cys Glu Gly Asn	
225 230 235	
atc acc att cca tgc agg ctt gct act gtt gca tca ggg gca gct tca	832
Ile Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser	
240 245 250	
ggg aaa ttt ctg gag tat gaa ctt ggg ggt ccc cgt gtt tgt gtc caa	880
Gly Lys Phe Leu Glu Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln	
255 260 265	

aca gct tat ggt ata gag gtt gag gtt gaa aac aac ccc tat gat cca	928
Thr Ala Tyr Gly Ile Glu Val Glu Val Glu Asn Asn Pro Tyr Asp Pro	
270 275 280	
gat cta atg gtg ttc atg gat tat aga gac ttc tca aaa cat aaa ccg	976
Asp Leu Met Val Phe Met Asp Tyr Arg Asp Phe Ser Lys His Lys Pro	
285 290 295 300	
gaa tct tta gaa gca aaa tat ccg act ttc ctc tat gtc atg gcc atg	1024
Glu Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu Tyr Val Met Ala Met	
305 310 315	
tct cca aca aaa ata ttc ttc gag gaa act tgt tta gct tca aga gaa	1072
Ser Pro Thr Lys Ile Phe Phe Glu Glu Thr Cys Leu Ala Ser Arg Glu	
320 325 330	
gcc atg cct ttc aat ctt cta aag tcc aaa ctc atg tca cga tta aag	1120
Ala Met Pro Phe Asn Leu Leu Lys Ser Lys Leu Met Ser Arg Leu Lys	
335 340 345	
gca atg ggt atc cga ata aca aga acg tac gaa gag gaa tgg tcg tat	1168
Ala Met Gly Ile Arg Ile Thr Arg Thr Tyr Glu Glu Glu Trp Ser Tyr	
350 355 360	
atc ccc gta ggt gga tcg tta cct aat aca gaa caa aag aat ctc gca	1216
Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala	
365 370 375 380	
ttt ggt gct gca gct agt atg gtg cac cct gcc aca ggg tat tca gtt	1264
Phe Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val	
385 390 395	
gtt cga tct ttg tca gaa gct cct aat tat gca gca gtc att gct aag	1312
Val Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys	
400 405 410	
att tta aga caa gat caa tct aaa gag atg att tct ctt gga aaa tac	1360
Ile Leu Arg Gln Asp Gln Ser Lys Glu Met Ile Ser Leu Gly Lys Tyr	
415 420 425	
act aac att tca aaa caa gca tgg gaa aca ttg tgg cca ctt gaa agg	1408
Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg	
430 435 440	
aaa aga cag cga gcc ttc ttt cta ttc gga cta tca cac atc gtg cta	1456
Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ser His Ile Val Leu	
445 450 455 460	
atg gat cta gag gga aca cgt aca ttt ttc cgt act ttc ttt cgt ttg	1504
Met Asp Leu Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu	
465 470 475	
ccc aaa tgg atg tgg tgg gga ttt ttg ggg tct tct tta tct tca acg	1552
Pro Lys Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr	
480 485 490	
gat ttg ata ata ttt gcg ctt tat atg ttt gtg ata gca cct cac agc	1600
Asp Leu Ile Ile Phe Ala Leu Tyr Met Phe Val Ile Ala Pro His Ser	
495 500 505	
ttg aga atg gaa ctg gtt aga cat cta ctt tct gat ccg aca ggg gca	1648
Leu Arg Met Glu Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Ala	
510 515 520	
act atg gta aaa gca tat ctc act ata tagatttaga ttatataaat	1695
Thr Met Val Lys Ala Tyr Leu Thr Ile	
525 530	

aatacccata tcttgcatat atataagcct tattttatttc ttttgtatcc ttacaacaac 1755
 atactcgtta attatatgtt tttta 1780

<210> 24

<211> 533

<212> PRT

<213> Lactuca sativa

<400> 24

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Thr	Cys	Pro	Arg	Phe	Thr	Asp	Cys	Asn	Ile	Arg	His	Lys	Phe	Ser	Leu		
			20					25					30				
Leu	Lys	Gln	Arg	Arg	Phe	Thr	Asn	Leu	Ser	Ala	Ser	Ser	Ser	Leu	Arg		
		35					40					45					
Gln	Ile	Lys	Cys	Ser	Ala	Lys	Ser	Asp	Arg	Cys	Val	Val	Asp	Lys	Gln		
	50					55					60						
Gly	Ile	Ser	Val	Ala	Asp	Glu	Glu	Asp	Tyr	Val	Lys	Ala	Gly	Gly	Ser		
65					70					75					80		
Glu	Leu	Phe	Phe	Val	Gln	Met	Gln	Arg	Thr	Lys	Ser	Met	Glu	Ser	Gln		
				85					90					95			
Ser	Lys	Leu	Ser	Glu	Lys	Leu	Ala	Gln	Ile	Pro	Ile	Gly	Asn	Cys	Ile		
			100					105					110				
Leu	Asp	Leu	Val	Val	Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala		
	115						120					125					
Ala	Glu	Ser	Ala	Lys	Leu	Gly	Leu	Asn	Val	Gly	Leu	Ile	Gly	Pro	Asp		
	130					135					140						
Leu	Pro	Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Gln	Asp	Glu	Phe	Ile	Gly		
145					150					155					160		
Leu	Gly	Leu	Glu	Gly	Cys	Ile	Glu	His	Ser	Trp	Lys	Asp	Thr	Leu	Val		
				165					170					175			
Tyr	Leu	Asp	Asp	Ala	Asp	Pro	Ile	Arg	Ile	Gly	Arg	Ala	Tyr	Gly	Arg		
		180						185					190				
Val	His	Arg	Asp	Leu	Leu	His	Glu	Glu	Leu	Leu	Arg	Arg	Cys	Val	Glu		
		195					200					205					
Ser	Gly	Val	Ser	Tyr	Leu	Ser	Ser	Lys	Val	Glu	Arg	Ile	Thr	Glu	Ala		
	210					215					220						
Pro	Asn	Gly	Tyr	Ser	Leu	Ile	Glu	Cys	Glu	Gly	Asn	Ile	Thr	Ile	Pro		
225					230					235					240		
Cys	Arg	Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Phe	Leu		
				245					250					255			
Glu	Tyr	Glu	Leu	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly		
			260					265					270				
Ile	Glu	Val	Glu	Val	Glu	Asn	Asn	Pro	Tyr	Asp	Pro	Asp	Leu	Met	Val		
	275					280						285					
Phe	Met	Asp	Tyr	Arg	Asp	Phe	Ser	Lys	His	Lys	Pro	Glu	Ser	Leu	Glu		
	290					295					300						
Ala	Lys	Tyr	Pro	Thr	Phe	Leu	Tyr	Val	Met	Ala	Met	Ser	Pro	Thr	Lys		
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<210> 25

<211> 1848

<212> DNA

<213> Adonis palaestina

<220>

<221> CDS

<222> (116)..(1702)

<223> coding for epsilon cyclase

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ccattttctt gttttctctt caaaacaaca aactaatgtg acggagtatc tagct atg 118
Met
1

gaa cta ctt ggt gtt cgc aac ctc atc tct tct tgc cct gtc tgg act 166
Glu Leu Leu Gly Val Arg Asn Leu Ile Ser Ser Cys Pro Val Trp Thr
5 10 15

ttt gga aca aga aac ctt agt agt tca aaa cta gct tat aac ata cat 214
Phe Gly Thr Arg Asn Leu Ser Ser Ser Lys Leu Ala Tyr Asn Ile His
20 25 30

cga	tat	ggg	tct	tct	tgt	aga	gta	gat	ttt	caa	gtg	agg	gct	gat	ggg	262
Arg	Tyr	Gly	Ser	Ser	Cys	Arg	Val	Asp	Phe	Gln	Val	Arg	Ala	Asp	Gly	
35						40					45					
gga	agc	ggg	agt	aga	act	tct	gtt	gct	tat	aaa	gag	ggg	ttt	gtg	gac	310
Gly	Ser	Gly	Ser	Arg	Thr	Ser	Val	Ala	Tyr	Lys	Glu	Gly	Phe	Val	Asp	
50					55					60					65	
gag	gag	gat	ttt	atc	aaa	gct	ggg	ggg	tct	gag	ctt	ttg	ttt	gtc	caa	358
Glu	Glu	Asp	Phe	Ile	Lys	Ala	Gly	Gly	Ser	Glu	Leu	Leu	Phe	Val	Gln	
				70					75					80		
atg	cag	caa	aca	aag	tct	atg	gag	aaa	cag	gcc	aag	ctc	gcc	gat	aag	406
Met	Gln	Gln	Thr	Lys	Ser	Met	Glu	Lys	Gln	Ala	Lys	Leu	Ala	Asp	Lys	
			85					90					95			
ttg	cca	cca	ata	cct	ttc	gga	gaa	tct	gtg	atg	gac	ttg	gtt	gta	ata	454
Leu	Pro	Pro	Ile	Pro	Phe	Gly	Glu	Ser	Val	Met	Asp	Leu	Val	Val	Ile	
	100						105					110				
ggg	tgt	gga	cct	gct	ggg	ctt	tca	ctg	gct	gca	gaa	gct	gct	aag	cta	502
Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ser	Leu	Ala	Ala	Glu	Ala	Ala	Lys	Leu	
	115					120					125					
ggc	ttg	aaa	gtt	ggc	ctt	att	ggg	cct	gat	ctt	cct	ttt	aca	aat	aat	550
Gly	Leu	Lys	Val	Gly	Leu	Ile	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	
130					135					140					145	
tat	ggg	gtg	tgg	gaa	gac	gag	ttc	aaa	gat	ctt	gga	ctt	gaa	cgt	tgt	598
Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Lys	Asp	Leu	Gly	Leu	Glu	Arg	Cys	
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Cys	Gly	Pro	Ala	Gly	Leu	Ser	Leu	Ala	Ala	Glu	Ala	Ala	Lys	Leu	Gly	
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 Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Thr Thr Trp Ser
 130 135 140
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 Gly Ala Val Val Tyr Val Asp Glu Gly Val Lys Lys Asp Leu Ser Arg
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Ser	Ser	Asn	Arg	Ile	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg	Pro	
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Ala	Glu	Val	Trp	Arg	Asp	Leu	Trp	Pro	Ile	Glu	Arg	Arg	Arg	Gln	Arg	
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Glu	Phe	Phe	Cys	Phe	Gly	Met	Asp	Ile	Leu	Leu	Lys	Leu	Asp	Leu	Asp	
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35

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 Trp His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu Val
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 Lys Glu Asn Leu Asp Phe Glu Leu Pro Leu Tyr Asp Thr Ser Lys Ser
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 Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile Asp
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 Gly Ala Val Val Tyr Val Asp Glu Gly Val Lys Lys Asp Leu Ser Arg
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 Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Leu Gln
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 Lys Cys Ile Thr Asn Gly Val Lys Phe His Gln Ser Lys Val Thr Asn
 180 185 190
 Val Val His Glu Glu Ala Asn Ser Thr Val Val Cys Ser Asp Gly Val
 195 200 205

36

Lys Ile Gln Ala Ser Val Val Leu Asp Ala Thr Gly Phe Ser Arg Cys
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 Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala Tyr
 225 230 235 240
 Gly Ile Ile Ala Glu Val Asp Gly His Pro Phe Asp Val Asp Lys Met
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 Val Phe Met Asp Trp Arg Asp Lys His Leu Asp Ser Tyr Pro Glu Leu
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 Lys Glu Arg Asn Ser Lys Ile Pro Thr Phe Leu Tyr Ala Met Pro Phe
 275 280 285
 Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg Pro
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 Gly Leu Arg Met Glu Asp Ile Gln Glu Arg Met Ala Ala Arg Leu Lys
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 His Leu Gly Ile Asn Val Lys Arg Ile Glu Glu Asp Glu Arg Cys Val
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 Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val Gly
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Leu	Gly	Leu	Asn	Val	Gly	Leu	Ile	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	
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Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Arg	Asp	Leu	Gly	Leu	Glu	Gly	
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Cys	Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Val	Val	Tyr	Ile	Asp	Glu	Asp	
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Glu	Pro	Ile	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Leu	
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Leu	Ser	Ser	Lys	Val	Glu	Ser	Ile	Thr	Glu	Ser	Thr	Ser	Gly	His	Arg	
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Leu	Val	Ala	Cys	Glu	His	Asp	Met	Ile	Val	Pro	Cys	Arg	Leu	Ala	Thr	
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Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Glu	Tyr	Glu	Val	Gly	
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Gly	Pro	Lys	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	
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Glu	Asn	Asn	Pro	Tyr	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	
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Asp	Cys	Thr	Lys	Gln	Glu	Val	Pro	Ser	Phe	Glu	Ser	Asp	Asn	Pro	Thr	
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Phe	Leu	Tyr	Val	Met	Pro	Met	Ser	Ser	Thr	Arg	Val	Phe	Phe	Glu	Glu	
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Thr	Cys	Leu	Ala	Ser	Lys	Asp	Gly	Leu	Arg	Phe	Asp	Ile	Leu	Lys	Lys	
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38

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Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn	
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aca gaa caa aga aac ctc gca ttt ggt gct gct gct agc atg gtg cat	920
Thr Glu Gln Arg Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His	
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cca gcc act ggc tac tca gta gtc aga tca ctg tca gag gct cca aac	968
Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Asn	
295 300 305	
tat gct tct gca att gca tat ata ttg aaa cac gat cat tcc aga ggt	1016
Tyr Ala Ser Ala Ile Ala Tyr Ile Leu Lys His Asp His Ser Arg Gly	
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Arg Leu Thr His Glu Gln Ser Asn Glu Asn Ile Ser Met Gln Ala Trp	
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aat act ctc tgg cca cag gaa agg aag cgc caa aga gct ttt ttc ctc	1112
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Leu Gly Ser Ser Leu Ser Ser Ala Asp Leu Ile Leu Phe Ala Phe Tyr	
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Leu	
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Ser	Arg	His	Leu	Leu	His	Glu	Glu	Leu	Leu	Arg	Arg	Cys	Val	Glu	Ser
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Tyr	Glu	Val	Gly	Gly	Pro	Lys	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly	Val
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Glu	Val	Glu	Val	Glu	Asn	Asn	Pro	Tyr	Asp	Pro	Ser	Leu	Met	Val	Phe
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Leu Asn Gly Val Thr Asp Asn Pro Cys Arg Lys Ala Met Asp Thr Leu
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Leu Lys Thr His Asn Lys Leu Glu Phe Leu Pro Gln Val His Gly Ala
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Leu Glu Lys Ser Ser Ser Leu Ser Ser Leu Lys Ile Gln Asn Gln Glu
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Gln	Lys	Cys	Ile	Thr	Asn	Gly	Val	Lys	Phe	His	Gln	Ala	Lys	Val	Ile	
				205					210					215		
aag	gtt	att	cat	gaa	gag	tcc	aaa	tct	ttg	ttg	att	tgc	aat	gat	ggg	784
Lys	Val	Ile	His	Glu	Glu	Ser	Lys	Ser	Leu	Leu	Ile	Cys	Asn	Asp	Gly	
			220					225					230			
gtg	aca	att	cag	gca	gcc	gtg	gtt	ctt	gat	gct	acg	ggg	ttc	tct	agg	832
Val	Thr	Ile	Gln	Ala	Ala	Val	Val	Leu	Asp	Ala	Thr	Gly	Phe	Ser	Arg	
			235					240					245			
tgt	ctt	gtc	cag	tat	gat	aag	ccc	tat	aat	cca	ggg	tac	caa	gtg	gca	880
Cys	Leu	Val	Gln	Tyr	Asp	Lys	Pro	Tyr	Asn	Pro	Gly	Tyr	Gln	Val	Ala	
			250			255					260					
tat	gga	ata	cta	gct	gag	gta	gaa	cag	cac	ccg	ttt	gat	tta	gac	aag	928
Tyr	Gly	Ile	Leu	Ala	Glu	Val	Glu	Gln	His	Pro	Phe	Asp	Leu	Asp	Lys	
				265		270			275						280	
atg	gtt	ttc	atg	gat	tgg	aga	gat	tcg	cat	ctg	aac	aac	aat	tcg	cag	976
Met	Val	Phe	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Asn	Asn	Asn	Ser	Gln	
				285					290					295		
ctc	aaa	gag	gca	aat	agc	aaa	att	cct	act	ttt	ctt	tat	gcc	atg	ccc	1024
Leu	Lys	Glu	Ala	Asn	Ser	Lys	Ile	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	
				300				305					310			
ttt	tcg	tca	aac	agg	ata	ttt	ctt	gaa	gag	act	tcg	cta	gtg	gcg	cgg	1072
Phe	Ser	Ser	Asn	Arg	Ile	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg	
			315				320						325			
cct	gga	gtg	cca	atg	aaa	gat	atc	cag	gaa	aga	atg	gtg	gct	aga	tta	1120
Pro	Gly	Val	Pro	Met	Lys	Asp	Ile	Gln	Glu	Arg	Met	Val	Ala	Arg	Leu	
				330		335					340					
aag	cac	tta	ggc	ata	aaa	gtt	aaa	agc	att	gaa	gag	gat	gag	cat	tgt	1168
Lys	His	Leu	Gly	Ile	Lys	Val	Lys	Ser	Ile	Glu	Glu	Asp	Glu	His	Cys	
				345		350				355					360	
gtc	att	ccg	atg	ggg	ggg	ccc	ctt	cca	gtg	ctt	cct	caa	aga	gtt	gtt	1216
Val	Ile	Pro	Met	Gly	Gly	Pro	Leu	Pro	Val	Leu	Pro	Gln	Arg	Val	Val	
				365					370						375	
gga	ata	ggg	ggg	acc	gct	ggg	atg	gtg	cac	cct	tca	act	ggc	tat	atg	1264
Gly	Ile	Gly	Gly	Thr	Ala	Gly	Met	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	
				380					385					390		
gtg	gca	agg	act	tta	gct	gcg	gct	cct	att	gtt	gca	aat	gca	atc	gtt	1312
Val	Ala	Arg	Thr	Leu	Ala	Ala	Ala	Pro	Ile	Val	Ala	Asn	Ala	Ile	Val	
				395			400						405			
cga	agc	ctc	agt	tct	gac	aga	agc	att	tca	gga	cac	aaa	ttg	tct	gct	1360
Arg	Ser	Leu	Ser	Ser	Asp	Arg	Ser	Ile	Ser	Gly	His	Lys	Leu	Ser	Ala	
				410		415						420				
gaa	gtt	tgg	aaa	gat	ttg	tgg	ccc	ata	gaa	agg	aga	agg	caa	agg	gag	1408
Glu	Val	Trp	Lys	Asp	Leu	Trp	Pro	Ile	Glu	Arg	Arg	Arg	Gln	Arg	Glu	
				425		430				435					440	
ttc	ttc	tgt	ttt	ggg	atg	gat	atc	ctg	ctc	aaa	ctt	gac	tta	cct	gcc	1456
Phe	Phe	Cys	Phe	Gly	Met	Asp	Ile	Leu	Leu	Lys	Leu	Asp	Leu	Pro	Ala	
				445					450					455		
act	agg	agg	ttt	ttc	gat	gct	ttt	ttt	gat	ctg	gag	cct	cgt	tat	tgg	1504
Thr	Arg	Arg	Phe	Phe	Asp	Ala	Phe	Phe	Asp	Leu	Glu	Pro	Arg	Tyr	Trp	
			460					465					470			

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cat ggt ttc tta tca tcg aga ttg ttt ctc ccc gag ctt tta gtt ttt 1552
His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Leu Val Phe
      475                      480                      485

ggg ctt tct cta ttc tca cat gcc tct aat act tct agg cta gag atc 1600
Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Leu Glu Ile
      490                      495                      500

atg gca aag gga act ctt cct ttg gtt aac atg atc aac aac ttg gta 1648
Met Ala Lys Gly Thr Leu Pro Leu Val Asn Met Ile Asn Asn Leu Val
      505                      510                      515                      520

caa gat aca gat taaggtagacc atgatagtta taatgtgctt aataactcat 1700
Gln Asp Thr Asp

gcactaatcg ttataaaac acttcaaatt agttttgatg tttatagctt attacatgaa 1760
ccaaagctta tgatagacgt gcttttggtat ttaagagttt cagccaaaaa aaaaaaaaaa 1820
aaaaaaaaaa 1830

<210> 34
<211> 524
<212> PRT
<213> Citrus X paradisi

<400> 34
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Phe Leu Pro Gln Val His Gly Ala Leu Glu Lys Ser Ser Ser Leu Ser
      35      40      45
Ser Leu Lys Ile Gln Asn Gln Glu Leu Arg Phe Gly Leu Lys Lys Ser
      50      55      60
Arg Gln Lys Arg Asn Arg Ser Cys Phe Ile Lys Ala Ser Ser Ser Ala
      65      70      75      80
Leu Leu Glu Leu Val Pro Glu Thr Lys Lys Glu Asn Leu Glu Phe Glu
      85      90      95
Leu Pro Met Tyr Asp Pro Ser Lys Gly Leu Val Val Asp Leu Ala Val
      100      105      110
Val Gly Gly Gly Pro Ala Gly Leu Ala Val Ala Gln Gln Val Ser Gly
      115      120      125
Ala Gly Leu Ser Val Cys Ser Ile Asp Pro Ser Pro Lys Leu Ile Trp
      130      135      140
Pro Asn Asn Tyr Gly Val Trp Val Asp Glu Phe Glu Ala Met Asp Leu
      145      150      155      160
Leu Asp Cys Leu Asp Thr Thr Trp Ser Gly Ala Val Val His Ile Asp
      165      170      175
Asp Asn Thr Lys Lys Asp Leu Asn Arg Pro Tyr Gly Arg Val Asn Arg
      180      185      190
Lys Leu Leu Lys Ser Lys Met Leu Gln Lys Cys Ile Thr Asn Gly Val
      195      200      205
Lys Phe His Gln Ala Lys Val Ile Lys Val Ile His Glu Glu Ser Lys
      210      215      220
Ser Leu Leu Ile Cys Asn Asp Gly Val Thr Ile Gln Ala Ala Val Val
      225      230      235      240

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15

44

att ggc ccg gat ctc cct ttc aca aac aat tat ggt gtg tgg gaa gat	97
Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp	
20 25 30	
gaa ttt aga gat ctt gga ctt gaa ggg tgt atc gaa caa gtc tgg aga	145
Glu Phe Arg Asp Leu Gly Leu Glu Gly Cys Ile Glu Gln Val Trp Arg	
35 40 45	
gac aca gtt gta tat att gat gaa gat gaa ccc atc ttg att ggt cgt	193
Asp Thr Val Val Tyr Ile Asp Glu Asp Glu Pro Ile Leu Ile Gly Arg	
50 55 60	
gct tat gga cga gtt agt cga cat ttg ctt cat gaa gaa tta tta aga	241
Ala Tyr Gly Arg Val Ser Arg His Leu Leu His Glu Glu Leu Leu Arg	
65 70 75 80	
agg tgt gtc gag tca ggt gta tca tat ctt agc tca aaa gtg gaa agc	289
Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Ser	
85 90 95	
att acg gaa tct acc agt ggt cat cgt ctt gta gct tgt gaa cat gat	337
Ile Thr Glu Ser Thr Ser Gly His Arg Leu Val Ala Cys Glu His Asp	
100 105 110	
atg att gtc ccc tgc agg ctt gct act gtt gct tct gga gca gca tca	385
Met Ile Val Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser	
115 120 125	
ggg aag cta ttg gaa tat ggg gtg ggg ggt ccc aaa gtt tct gtc caa	433
Gly Lys Leu Leu Glu Tyr Gly Val Gly Gly Pro Lys Val Ser Val Gln	
130 135 140	
aca gct tat ggt gtg gag gtt gag gtg gaa aat aat cca tat gat cca	481
Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn Asn Pro Tyr Asp Pro	
145 150 155 160	
agc ctt atg gtt ttc atg gac tac aga gac tgt act aag caa gaa gtt	529
Ser Leu Met Val Phe Met Asp Tyr Arg Asp Cys Thr Lys Gln Glu Val	
165 170 175	
cca tct ttt gaa tct gac aat cca aca ttt ctt tat gtc atg ccc atg	577
Pro Ser Phe Glu Ser Asp Asn Pro Thr Phe Leu Tyr Val Met Pro Met	
180 185 190	
tct tca aca aga gtt ttc ttt gag gaa act tgt ttg gca tcg aaa gat	625
Ser Ser Thr Arg Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Asp	
195 200 205	
ggc tta cgt ttt gac ata ttg aag aaa aag ctc atg gca agg tta gag	673
Gly Leu Arg Phe Asp Ile Leu Lys Lys Lys Leu Met Ala Arg Leu Glu	
210 215 220	
aga ttg gga atc cag gtt ttg aaa act tat gaa gag gaa tgg tca tat	721
Arg Leu Gly Ile Gln Val Leu Lys Thr Tyr Glu Glu Glu Trp Ser Tyr	
225 230 235 240	
att cca gtt ggt ggt tcc tta cca aat aca gaa caa aga aac ctc gca	769
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245 250 255	
tat ggt gct gct gct agc	787
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<210> 36

<211> 262

<212> PRT

<213> Citrus sinensis

<400> 36

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          20              25              30
Glu Phe Arg Asp Leu Gly Leu Glu Gly Cys Ile Glu Gln Val Trp Arg
          35              40              45
Asp Thr Val Val Tyr Ile Asp Glu Asp Glu Pro Ile Leu Ile Gly Arg
          50              55              60
Ala Tyr Gly Arg Val Ser Arg His Leu Leu His Glu Glu Leu Leu Arg
          65              70              75              80
Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Ser
          85              90              95
Ile Thr Glu Ser Thr Ser Gly His Arg Leu Val Ala Cys Glu His Asp
          100             105             110
Met Ile Val Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser
          115             120             125
Gly Lys Leu Leu Glu Tyr Gly Val Gly Gly Pro Lys Val Ser Val Gln
          130             135             140
Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn Asn Pro Tyr Asp Pro
          145             150             155             160
Ser Leu Met Val Phe Met Asp Tyr Arg Asp Cys Thr Lys Gln Glu Val
          165             170             175
Pro Ser Phe Glu Ser Asp Asn Pro Thr Phe Leu Tyr Val Met Pro Met
          180             185             190
Ser Ser Thr Arg Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Asp
          195             200             205
Gly Leu Arg Phe Asp Ile Leu Lys Lys Lys Leu Met Ala Arg Leu Glu
          210             215             220
Arg Leu Gly Ile Gln Val Leu Lys Thr Tyr Glu Glu Glu Trp Ser Tyr
          225             230             235             240
Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Arg Asn Leu Ala
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Tyr Gly Ala Ala Ala Ser
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<210> 37

<211> 2357

<212> DNA

<213> Spinacia oleracea

<220>

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<222> (264)..(1814)

<223> coding for epsilon-cyclase

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cactgaactt caccactaca aacttaaaaa aaatcttggg gaaatttgat tccgtaaaaa 180
tggagtatta ttgtctcgga gcttcgaaat tcgcaacaat ggcggtttct cctgcgctta 240
atcacgacaa tttgaggaat aaa atg gtt aaa caa cgc cag aat ttc cag acg 293
Met Val Lys Gln Arg Gln Asn Phe Gln Thr
      1              5              10
ttt tgc ttt tgg agg ccg aat tct tcg aac gtt gta gta gaa tgt agt 341
Phe Cys Phe Trp Arg Pro Asn Ser Ser Asn Val Val Val Glu Cys Ser
      15              20              25
agt cgt agg agt gga agt agt gtt ttg agg agt gcg aat agc gac agt 389
Ser Arg Arg Ser Gly Ser Ser Val Leu Arg Ser Ala Asn Ser Asp Ser
      30              35              40
agt tgc gta att gcg cca gag gat ttt gcg aac gaa gaa gat ttc atc 437
Ser Cys Val Ile Ala Pro Glu Asp Phe Ala Asn Glu Glu Asp Phe Ile
      45              50              55
aaa gct ggt ggt tcc gag ctt ctt tat gtt caa atg cag cag aat aaa 485
Lys Ala Gly Gly Ser Glu Leu Leu Tyr Val Gln Met Gln Gln Asn Lys
      60              65              70
gct atg gat tgt tac tcc aaa att tcc gat aag ctg cgt caa ata tca 533
Ala Met Asp Cys Tyr Ser Lys Ile Ser Asp Lys Leu Arg Gln Ile Ser
      75              80              85              90
gat gcc aat gaa ctg ctg gat atg gtg gtt att ggt tgt ggt cca gct 581
Asp Ala Asn Glu Leu Leu Asp Met Val Val Ile Gly Cys Gly Pro Ala
      95              100              105
ggt cta gct ttg gct gca gaa tcg gct aaa ctt gga tta aaa gtt ggc 629
Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly Leu Lys Val Gly
      110              115              120
ctt gtt ggt cct gat ctt cct ttt acg aat aac tac ggc gtt tgg gaa 677
Leu Val Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu
      125              130              135
gat gaa ttc aga gca ttg gga ctt gga ggc tgt atc gag cac gtt tgg 725
Asp Glu Phe Arg Ala Leu Gly Leu Gly Gly Cys Ile Glu His Val Trp
      140              145              150
cgt gat acc att gtg tat att gat gat gac aat cct ata tat att ggt 773
Arg Asp Thr Ile Val Tyr Ile Asp Asp Asp Asn Pro Ile Tyr Ile Gly
      155              160              165              170
cga tct tat gga aaa gtc agc cgg caa tta ctt cac aag gaa ctg gtg 821
Arg Ser Tyr Gly Lys Val Ser Arg Gln Leu Leu His Lys Glu Leu Val
      175              180              185
cac agg tgt ttg gag tca ggt gtc tct tat ctg aat gcg aaa gtg gaa 869
His Arg Cys Leu Glu Ser Gly Val Ser Tyr Leu Asn Ala Lys Val Glu
      190              195              200
aat att atg gaa gga cct gat gga cat agg ctt gtt gct tgt gaa cgt 917
Asn Ile Met Glu Gly Pro Asp Gly His Arg Leu Val Ala Cys Glu Arg
      205              210              215
ggt gtc act att ccc tgc agg ctt gta act gtt gca tct gga gca gct 965
Gly Val Thr Ile Pro Cys Arg Leu Val Thr Val Ala Ser Gly Ala Ala
      220              225              230
tca ggg aaa ctt ctg gag tat gaa gtg ggt ggt cca agg gtt tgt gta 1013
Ser Gly Lys Leu Leu Glu Tyr Glu Val Gly Gly Pro Arg Val Cys Val
      235              240              245              250

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Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	Asn	Ser	Pro	Tyr	Asp	
				255					260					265		
ccc	aat	gtg	atg	gtg	ttc	atg	gac	tac	aga	gac	tac	act	aaa	ctg	agc	1109
Pro	Asn	Val	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Tyr	Thr	Lys	Leu	Ser	
			270					275					280			
gtt	caa	tct	ctg	gag	gca	aag	tat	cca	aca	ttc	ttg	tat	gca	atg	ccg	1157
Val	Gln	Ser	Leu	Glu	Ala	Lys	Tyr	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	
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ata	tca	cca	act	agg	atc	ttc	ttt	gag	gag	act	tgc	ttg	gct	tca	gta	1205
Ile	Ser	Pro	Thr	Arg	Ile	Phe	Phe	Glu	Glu	Thr	Cys	Leu	Ala	Ser	Val	
	300					305					310					
gat	gca	atg	ccc	ttt	gac	ctg	ctc	aag	aaa	aag	ctt	atg	aca	aga	tta	1253
Asp	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Lys	Lys	Leu	Met	Thr	Arg	Leu	
315					320					325					330	
caa	act	atg	ggt	gtt	cgt	atc	acc	aaa	ata	tat	gaa	gag	gag	tgg	tct	1301
Gln	Thr	Met	Gly	Val	Arg	Ile	Thr	Lys	Ile	Tyr	Glu	Glu	Glu	Trp	Ser	
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tat	ata	cct	gtt	ggt	ggg	tcc	tta	cca	aat	aca	gag	caa	aga	aac	ctt	1349
Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Glu	Gln	Arg	Asn	Leu	
			350					355					360			
gca	ttt	ggt	gct	gct	gcg	agc	atg	gtg	cat	cca	gcc	aca	ggt	tat	tca	1397
Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala	Thr	Gly	Tyr	Ser	
		365					370					375				
gtc	gtg	aga	tca	ctg	tca	gaa	gct	cca	aag	tat	gct	tct	gca	att	gca	1445
Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys	Tyr	Ala	Ser	Ala	Ile	Ala	
	380					385					390					
aac	ttg	atc	aag	aat	gac	ctg	tca	aaa	aat	gca	ata	ttg	cgt	cag	agg	1493
Asn	Leu	Ile	Lys	Asn	Asp	Leu	Ser	Lys	Asn	Ala	Ile	Leu	Arg	Gln	Arg	
395					400					405					410	
agt	gtg	ggg	aat	atc	tca	atg	caa	gcc	tgg	aat	act	ctt	tgg	cca	caa	1541
Ser	Val	Gly	Asn	Ile	Ser	Met	Gln	Ala	Trp	Asn	Thr	Leu	Trp	Pro	Gln	
			415						420				425			
gaa	agg	aaa	cgt	cag	aga	gca	ttc	ttc	ctg	ttc	gga	cta	tca	ctt	ata	1589
Glu	Arg	Lys	Arg	Gln	Arg	Ala	Phe	Phe	Leu	Phe	Gly	Leu	Ser	Leu	Ile	
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gtc	cag	ctt	gat	att	gag	ggt	atc	agg	aca	ttc	ttc	cgc	acc	ttc	ttc	1637
Val	Gln	Leu	Asp	Ile	Glu	Gly	Ile	Arg	Thr	Phe	Phe	Arg	Thr	Phe	Phe	
		445					450					455				
cga	gtg	cca	aaa	tgg	atg	tgg	gag	gga	ttc	ctc	ggt	tct	aat	ctc	tct	1685
Arg	Val	Pro	Lys	Trp	Met	Trp	Glu	Gly	Phe	Leu	Gly	Ser	Asn	Leu	Ser	
	460					465					470					
tca	gct	gat	ctc	ata	ttg	ttt	gcc	ttt	tat	atg	ttc	ttt	att	gct	ccg	1733
Ser	Ala	Asp	Leu	Ile	Leu	Phe	Ala	Phe	Tyr	Met	Phe	Phe	Ile	Ala	Pro	
	475				480				485					490		
aat	gac	ttg	aga	atg	ggt	ctt	ata	agg	cat	cta	cta	tct	gat	cct	aca	1781
Asn	Asp	Leu	Arg	Met	Gly	Leu	Ile	Arg	His	Leu	Leu	Ser	Asp	Pro	Thr	
				495					500					505		
ggg	gcg	acc	atg	ata	aga	acg	tac	ata	aca	cta	taaaagtaat atgaaatgct					1834
Gly	Ala	Thr	Met	Ile	Arg	Thr	Tyr	Ile	Thr	Leu						
			510					515								

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 gtgtaaaaaa aacacaatta ataaattttt tgtagggtgca gcctctatac ttgatattct 1954
 cgattcagat ataattattgt cagtattctt cgtaaagat cagttgtttc tacaattcca 2014
 gaggtcctg gaattggtgt tacccttcca tgtagctcat tgataaatgt tgagggtaga 2074
 ggctttttct tagatgcttg cttgcagctt gctcatggat atattcagtt gttcagtaga 2134
 cacgttaaca actactacag tggggggcatc attgatctgg accgggagag ctgagcatct 2194
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 cagctgatgg ggttcaccct gtaaggtagag tttcttacca actccaccaa cttatgttgg 2314
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<210> 38

<211> 517

<212> PRT

<213> *Spinacia oleracea*

<400> 38

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Ser	Val	Leu	Arg	Ser	Ala	Asn	Ser	Asp	Ser	Ser	Cys	Val	Ile	Ala	Pro	35	40	45	
Glu	Asp	Phe	Ala	Asn	Glu	Glu	Asp	Phe	Ile	Lys	Ala	Gly	Gly	Ser	Glu	50	55	60	
Leu	Leu	Tyr	Val	Gln	Met	Gln	Gln	Asn	Lys	Ala	Met	Asp	Cys	Tyr	Ser	65	70	75	80
Lys	Ile	Ser	Asp	Lys	Leu	Arg	Gln	Ile	Ser	Asp	Ala	Asn	Glu	Leu	Leu	85	90	95	
Asp	Met	Val	Val	Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	100	105	110	
Glu	Ser	Ala	Lys	Leu	Gly	Leu	Lys	Val	Gly	Leu	Val	Gly	Pro	Asp	Leu	115	120	125	
Pro	Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Arg	Ala	Leu	130	135	140	
Gly	Leu	Gly	Gly	Cys	Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Ile	Val	Tyr	145	150	155	160
Ile	Asp	Asp	Asp	Asn	Pro	Ile	Tyr	Ile	Gly	Arg	Ser	Tyr	Gly	Lys	Val	165	170	175	
Ser	Arg	Gln	Leu	Leu	His	Lys	Glu	Leu	Val	His	Arg	Cys	Leu	Glu	Ser	180	185	190	
Gly	Val	Ser	Tyr	Leu	Asn	Ala	Lys	Val	Glu	Asn	Ile	Met	Glu	Gly	Pro	195	200	205	
Asp	Gly	His	Arg	Leu	Val	Ala	Cys	Glu	Arg	Gly	Val	Thr	Ile	Pro	Cys	210	215	220	
Arg	Leu	Val	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Glu	225	230	235	240
Tyr	Glu	Val	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	245	250	255	


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<210> 39
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<212> DNA
<213> Solanum tuberosum
<220>
<221> CDS
<222> (2)..(1147)
<223> coding for episilon-cyclase      (partial)
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t agc ggn nnn nag gat gag ttc aaa gat ctt ggt ctt caa gcc tgc att 49
  Ser Xaa Xaa Xaa Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys Ile
      1             5             10             15
gaa cat gtt tgg cgg gat acc att gta tat ctt gat gat gat gat cct 97
Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Asp Pro
      20             25             30

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50

att ctt att ggc cgt gcc tat gga aga gtt agt cgc cat tta ctg cac	145
Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu His	
35 40 45	
gag gag tta ctc aaa agg tgt gtg gag gca ggt gtt ttg tat cta aac	193
Glu Glu Leu Leu Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn	
50 55 60	
tcg aaa gtg gat agg att gtt gag gcc aca aat ggc cac agt ctt gta	241
Ser Lys Val Asp Arg Ile Val Glu Ala Thr Asn Gly His Ser Leu Val	
65 70 75 80	
gag tgc gag ggt gat gtt gtg att ccc tgc agg ttt gtg act gtt gca	289
Glu Cys Glu Gly Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala	
85 90 95	
tcg gga gca gcc tcg ggg aaa ttc ttg cag tat gag ttg gga ggt cct	337
Ser Gly Ala Ala Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Gly Pro	
100 105 110	
aga gtt tct gtt caa aca gct tat gga gtg gaa gtt gag gtc gat aac	385
Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn	
115 120 125	
aat cca ttt gac ccg agc ctg atg gtt ttc atg gat tat aga gac tat	433
Asn Pro Phe Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr	
130 135 140	
gtc aga cac gac gct caa tct tta gaa gct aaa tat cca aca ttt ctc	481
Val Arg His Asp Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu	
145 150 155 160	
tat gcc atg ccc atg tct cca aca cga gtc ttt ttc gag gaa act tgt	529
Tyr Ala Met Pro Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys	
165 170 175	
ttg gct tca aaa gat gca atg cca ttc gat ctg tta aag aaa aaa ttg	577
Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu	
180 185 190	
atg tta cga ttg aac acc ctc ggt gta aga att aaa gaa att tat gag	625
Met Leu Arg Leu Asn Thr Leu Gly Val Arg Ile Lys Glu Ile Tyr Glu	
195 200 205	
gag gaa tgg tct tac ata cca gtt gga gga tct ttg cca aat aca gaa	673
Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu	
210 215 220	
caa aaa aca ctt gca ttt ggt gct gct gct agc atg gtt cat cca gcc	721
Gln Lys Thr Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala	
225 230 235 240	
aca ggt tat tca gtc gtc aga tca ctg tct gaa gct cca aaa tgc gcc	769
Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys Ala	
245 250 255	
ttc gtg ctt gca aat ata tta cga caa aat cat agc aag aat atg ctt	817
Phe Val Leu Ala Asn Ile Leu Arg Gln Asn His Ser Lys Asn Met Leu	
260 265 270	
act agt tca agt acc ccg agt att tca act caa gct tgg aac act ctt	865
Thr Ser Ser Ser Thr Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr Leu	
275 280 285	
tgg cca caa gaa cga aaa cga caa aga tcg ttt ttc cta ttt gga ctg	913
Trp Pro Gln Glu Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly Leu	
290 295 300	

51

gct ctg ata ttg cag ctg gat att gag ggg ata agg tca ttt ttc cgc 961
 Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe Arg
 305 310 315 320
 gcg ttc ttc cgt gtg cca aaa tgg atg tgg cag gga ttt ctt ggt tca 1009
 Ala Phe Phe Arg Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser
 325 330 335
 agt ctt tct tna gca gac ctc atg tta ttt gcc ttc tac atg ttt att 1057
 Ser Leu Ser Xaa Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe Ile
 340 345 350
 att gca cca aat gac atg aga aga ggc tta atc aga cat ctt tta tct 1105
 Ile Ala Pro Asn Asp Met Arg Arg Gly Leu Ile Arg His Leu Leu Ser
 355 360 365
 gat cct act ggt gca aca ttg ata aga act tat ctt aca ttt 1147
 Asp Pro Thr Gly Ala Thr Leu Ile Arg Thr Tyr Leu Thr Phe
 370 375 380
 tagagtaaata tcctcctaca atagttgttg aannagaggc ctcattactt cagattcata 1207
 acagaaatcg cggctctctcg aggccttgta tataacattt tcactagggtt aatattgctt 1267
 gaataagttg cacagttttca gtttttgtat ctgcttcttt tttgtccaag atcatgtatt 1327
 ganccaattt atatacattg ccagtatata taaattttat aaaaaaaaaa a 1378
 <210> 40
 <211> 382
 <212> PRT
 <213> Solanum tuberosum
 <400> 40
 Ser Xaa Xaa Xaa Asp Glu Phe Lys Asp Leu Gly Leu Gln Ala Cys Ile
 1 5 10 15
 Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Asp Asp Pro
 20 25 30
 Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu His
 35 40 45
 Glu Glu Leu Leu Lys Arg Cys Val Glu Ala Gly Val Leu Tyr Leu Asn
 50 55 60
 Ser Lys Val Asp Arg Ile Val Glu Ala Thr Asn Gly His Ser Leu Val
 65 70 75 80
 Glu Cys Glu Gly Asp Val Val Ile Pro Cys Arg Phe Val Thr Val Ala
 85 90 95
 Ser Gly Ala Ala Ser Gly Lys Phe Leu Gln Tyr Glu Leu Gly Gly Pro
 100 105 110
 Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Asp Asn
 115 120 125
 Asn Pro Phe Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr
 130 135 140
 Val Arg His Asp Ala Gln Ser Leu Glu Ala Lys Tyr Pro Thr Phe Leu
 145 150 155 160
 Tyr Ala Met Pro Met Ser Pro Thr Arg Val Phe Phe Glu Glu Thr Cys
 165 170 175
 Leu Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu
 180 185 190

52

Met	Leu	Arg	Leu	Asn	Thr	Leu	Gly	Val	Arg	Ile	Lys	Glu	Ile	Tyr	Glu
		195					200					205			
Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Glu
	210					215					220				
Gln	Lys	Thr	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala
225					230					235					240
Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys	Cys	Ala
				245					250					255	
Phe	Val	Leu	Ala	Asn	Ile	Leu	Arg	Gln	Asn	His	Ser	Lys	Asn	Met	Leu
			260					265					270		
Thr	Ser	Ser	Ser	Thr	Pro	Ser	Ile	Ser	Thr	Gln	Ala	Trp	Asn	Thr	Leu
		275					280					285			
Trp	Pro	Gln	Glu	Arg	Lys	Arg	Gln	Arg	Ser	Phe	Phe	Leu	Phe	Gly	Leu
	290					295					300				
Ala	Leu	Ile	Leu	Gln	Leu	Asp	Ile	Glu	Gly	Ile	Arg	Ser	Phe	Phe	Arg
305					310					315					320
Ala	Phe	Phe	Arg	Val	Pro	Lys	Trp	Met	Trp	Gln	Gly	Phe	Leu	Gly	Ser
				325					330					335	
Ser	Leu	Ser	Xaa	Ala	Asp	Leu	Met	Leu	Phe	Ala	Phe	Tyr	Met	Phe	Ile
			340					345					350		
Ile	Ala	Pro	Asn	Asp	Met	Arg	Arg	Gly	Leu	Ile	Arg	His	Leu	Leu	Ser
		355					360					365			
Asp	Pro	Thr	Gly	Ala	Thr	Leu	Ile	Arg	Thr	Tyr	Leu	Thr	Phe		
	370					375					380				

<210> 41

<211> 497

<212> DNA

<213> Daucus carota

<220>

<221> CDS

<222> (1)..(495)

<223> coding for episilon-cyclase (partial)

<400> 41

tat	ggt	gtt	tgg	gtg	gat	gaa	ttt	ata	gat	ctt	gga	ctt	gaa	ggg	tgt	48
Tyr	Gly	Val	Trp	Val	Asp	Glu	Phe	Ile	Asp	Leu	Gly	Leu	Glu	Gly	Cys	
1				5					10					15		
att	gag	cat	gtt	tgg	cgg	gat	act	att	gta	tat	ctt	gat	gat	ggg	gat	96
Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Asp	Gly	Asp	
			20					25					30			
cct	att	atg	att	ggc	cgt	gct	tac	gga	aga	gtt	agt	cgc	cat	ttg	ctt	144
Pro	Ile	Met	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Leu	Leu	
		35				40						45				
cat	gaa	gaa	ttg	ctt	aaa	agg	tgt	gtc	gag	tca	ggg	gtt	tcg	tat	ctt	192
His	Glu	Glu	Leu	Leu	Lys	Arg	Cys	Val	Glu	Ser	Gly	Val	Ser	Tyr	Leu	
	50					55					60					
agc	tca	aaa	gtt	gaa	aag	att	att	gaa	gct	gga	gat	ggc	cac	agc	ctg	240
Ser	Ser	Lys	Val	Glu	Lys	Ile	Ile	Glu	Ala	Gly	Asp	Gly	His	Ser	Leu	
65					70					75					80	

53

```

gtt gag tgt gaa aat aat att gtc att cca tgc agg ctt gct act gtt 288
Val Glu Cys Glu Asn Asn Ile Val Ile Pro Cys Arg Leu Ala Thr Val
      85                      90                      95

gca tct gga gca gct tct ggg aaa ctt ttg cag tat gag gtt ggg ggt 336
Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly
      100                      105                      110

ccc aga gtt tct gtc caa aca gct tat ggt gtc gag gtt gag gtg gaa 384
Pro Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu
      115                      120                      125

aac aat cca tat gat ccc agt cta atg gtt ttc atg gat tac aga gat 432
Asn Asn Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp
      130                      135                      140

tat acc aaa caa aaa gtt cca ggc atg gag gca gaa tat cca act ttc 480
Tyr Thr Lys Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe
      145                      150                      155                      160

ctg tat gcc atg cca tt
Leu Tyr Ala Met Pro
      165

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<210> 42

<211> 165

<212> PRT

<213> Daucus carota

<400> 42

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Tyr Gly Val Trp Val Asp Glu Phe Ile Asp Leu Gly Leu Glu Gly Cys
  1                      5                      10                      15

Ile Glu His Val Trp Arg Asp Thr Ile Val Tyr Leu Asp Asp Gly Asp
      20                      25                      30

Pro Ile Met Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg His Leu Leu
      35                      40                      45

His Glu Glu Leu Leu Lys Arg Cys Val Glu Ser Gly Val Ser Tyr Leu
      50                      55                      60

Ser Ser Lys Val Glu Lys Ile Ile Glu Ala Gly Asp Gly His Ser Leu
      65                      70                      75                      80

Val Glu Cys Glu Asn Asn Ile Val Ile Pro Cys Arg Leu Ala Thr Val
      85                      90                      95

Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly
      100                      105                      110

Pro Arg Val Ser Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu
      115                      120                      125

Asn Asn Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp
      130                      135                      140

Tyr Thr Lys Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe
      145                      150                      155                      160

Leu Tyr Ala Met Pro
      165

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<210> 43

<211> 605

<212> DNA

<213> Daucus carota

<220>

<221> CDS

<222> (3)..(605)

<223> coding for episilon-cyclase (partial)

<400> 43

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tc att ggc cgt gct tat gga aga tta gtc gcc att tgc ttc atg aag      47
  Ile Gly Arg Ala Tyr Gly Arg Leu Val Ala Ile Cys Phe Met Lys
    1             5             10             15

aat tgc tta aaa ggt gtg tcg agt cag gtg ttt cgt atc tta gct caa      95
Asn Cys Leu Lys Gly Val Ser Ser Gln Val Phe Arg Ile Leu Ala Gln
                20             25             30

aag ttg aaa aga tta ttg aag ctg gag atg gcc aca gcc tgg ttg agt     143
Lys Leu Lys Arg Leu Leu Lys Leu Glu Met Ala Thr Ala Trp Leu Ser
                35             40             45

gtg aaa ata ata ttg tca ttc cat gca ggc ttg cta ctg ttg cat ctg     191
Val Lys Ile Ile Leu Ser Phe His Ala Gly Leu Leu Leu Leu His Leu
                50             55             60

gag cag ctt ctg gga aac ttt tgc agt atg ggg ttg ggg gtc cca gag     239
Glu Gln Leu Leu Gly Asn Phe Cys Ser Met Gly Leu Gly Val Pro Glu
                65             70             75

ttt ctg tcc aaa cag ctt atg gtg tcg agg ttg agg tgg aaa cca atc     287
Phe Leu Ser Lys Gln Leu Met Val Ser Arg Leu Arg Trp Lys Pro Ile
                80             85             90             95

cca tat gat ccc agt cta atg gtt ttc atg gat tac aga gat tat acc     335
Pro Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr
                100            105            110

aaa caa aaa gtt cca ggc atg gag gca gaa tat cca aca ttt ctt tat     383
Lys Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe Leu Tyr
                115            120            125

gtg atg ccc atg tcc cca aca agg att ttc ttt gag gag aca tgt ttg     431
Val Met Pro Met Ser Pro Thr Arg Ile Phe Phe Glu Glu Thr Cys Leu
                130            135            140

gct tca aaa gat gcg atg cca ttc gat cta ctg aag aaa aaa ctc atg     479
Ala Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met
                145            150            155

tca aga tta cag acg atg gga att cga gtt gcc aag aca tat gaa gag     527
Ser Arg Leu Gln Thr Met Gly Ile Arg Val Ala Lys Thr Tyr Glu Glu
                160            165            170            175

gaa tgg tct tat ata cct gtt ggg gga tct tta cct aat act gag caa     575
Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln
                180            185            190

aag aat ctc gcc ttt ggt gct gcc gct aga                               605
Lys Asn Leu Ala Phe Gly Ala Ala Ala Arg
                195            200

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<210> 44

<211> 201

<212> PRT

<213> Daucus carota

<400> 44

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Ile Gly Arg Ala Tyr Gly Arg Leu Val Ala Ile Cys Phe Met Lys Asn
  1             5             10             15

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55

Cys Leu Lys Gly Val Ser Ser Gln Val Phe Arg Ile Leu Ala Gln Lys
 20 25 30
 Leu Lys Arg Leu Leu Lys Leu Glu Met Ala Thr Ala Trp Leu Ser Val
 35 40 45
 Lys Ile Ile Leu Ser Phe His Ala Gly Leu Leu Leu Leu His Leu Glu
 50 55 60
 Gln Leu Leu Gly Asn Phe Cys Ser Met Gly Leu Gly Val Pro Glu Phe
 65 70 75 80
 Leu Ser Lys Gln Leu Met Val Ser Arg Leu Arg Trp Lys Pro Ile Pro
 85 90 95
 Tyr Asp Pro Ser Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys
 100 105 110
 Gln Lys Val Pro Gly Met Glu Ala Glu Tyr Pro Thr Phe Leu Tyr Val
 115 120 125
 Met Pro Met Ser Pro Thr Arg Ile Phe Phe Glu Glu Thr Cys Leu Ala
 130 135 140
 Ser Lys Asp Ala Met Pro Phe Asp Leu Leu Lys Lys Lys Leu Met Ser
 145 150 155 160
 Arg Leu Gln Thr Met Gly Ile Arg Val Ala Lys Thr Tyr Glu Glu Glu
 165 170 175
 Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys
 180 185 190
 Asn Leu Ala Phe Gly Ala Ala Ala Arg
 195 200

<210> 45

<211> 1697

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (6)..(1583)

<223> coding for epsilon-cyclase

<400> 45

ttgaa atg gag tgt gtt gga gtt caa aat gtt gga gca atg gca gtt tta 50
 Met Glu Cys Val Gly Val Gln Asn Val Gly Ala Met Ala Val Leu
 1 5 10 15
 acg cgt ccg aga ttg aac cgt tgg tcg gga gga gag tta tgc caa gaa 98
 Thr Arg Pro Arg Leu Asn Arg Trp Ser Gly Gly Glu Leu Cys Gln Glu
 20 25 30
 aaa agc atc ttt ttg gcg tat gag cag tat gaa agt aaa tgt aat agc 146
 Lys Ser Ile Phe Leu Ala Tyr Glu Gln Tyr Glu Ser Lys Cys Asn Ser
 35 40 45
 agt agt ggt agt gac agt tgt gta gtt gat aaa gaa gat ttt gct gat 194
 Ser Ser Gly Ser Asp Ser Cys Val Val Asp Lys Glu Asp Phe Ala Asp
 50 55 60
 gaa gaa gat tat ata aaa gcc ggt ggt tcg caa ctt gta ttt gtt caa 242
 Glu Glu Asp Tyr Ile Lys Ala Gly Gly Ser Gln Leu Val Phe Val Gln
 65 70 75

56

atg	cag	cag	aaa	aaa	gat	atg	gat	cag	cag	tct	aag	ctt	tct	gat	gag	290
Met	Gln	Gln	Lys	Lys	Asp	Met	Asp	Gln	Gln	Ser	Lys	Leu	Ser	Asp	Glu	
80					85					90					95	
tta	cga	caa	ata	tct	gct	gga	caa	acc	gta	ctg	gat	tta	gtg	gta	atc	338
Leu	Arg	Gln	Ile	Ser	Ala	Gly	Gln	Thr	Val	Leu	Asp	Leu	Val	Val	Ile	
			100						105					110		
ggc	tgt	ggt	cct	gct	ggt	ctt	gct	ctt	gcc	gcg	gag	tca	gct	aaa	ttg	386
Gly	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	Glu	Ser	Ala	Lys	Leu	
			115					120					125			
ggg	ttg	aac	gtg	ggg	ctc	gtt	ggg	cct	gat	ctt	cct	ttc	aca	aac	aac	434
Gly	Leu	Asn	Val	Gly	Leu	Val	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	
		130					135					140				
tat	ggt	gta	tgg	gag	gac	gag	ttc	aaa	gat	ctt	ggt	ctt	caa	gcc	tgc	482
Tyr	Gly	Val	Trp	Glu	Asp	Glu	Phe	Lys	Asp	Leu	Gly	Leu	Gln	Ala	Cys	
	145					150					155					
att	gaa	cat	gtt	tgg	cgg	gat	acc	att	gta	tat	ctt	gat	gat	gat	gaa	530
Ile	Glu	His	Val	Trp	Arg	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Asp	Asp	Glu	
160					165					170					175	
cct	att	ctt	att	ggc	cgt	gcc	tat	gga	aga	gtt	agt	cgc	cat	ttt	ctg	578
Pro	Ile	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Phe	Leu	
				180				185						190		
cac	gag	gag	tta	ctc	aaa	agg	tgt	gtg	gag	gca	ggt	gtt	ttg	tat	cta	626
His	Glu	Glu	Leu	Leu	Lys	Arg	Cys	Val	Glu	Ala	Gly	Val	Leu	Tyr	Leu	
			195					200					205			
aac	tcg	aaa	gtg	gat	agg	att	gtt	gag	gcc	aca	aat	ggc	cag	agt	ctt	674
Asn	Ser	Lys	Val	Asp	Arg	Ile	Val	Glu	Ala	Thr	Asn	Gly	Gln	Ser	Leu	
		210					215					220				
gta	gag	tgc	gaa	ggt	gat	gtt	gtg	att	ccc	tgc	agg	ttt	gtg	act	gtt	722
Val	Glu	Cys	Glu	Gly	Asp	Val	Val	Ile	Pro	Cys	Arg	Phe	Val	Thr	Val	
		225				230					235					
gca	tcg	ggg	gca	gcc	tcg	ggg	aaa	ttc	ttg	cag	tat	gag	ttg	gga	agt	770
Ala	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Phe	Leu	Gln	Tyr	Glu	Leu	Gly	Ser	
240				245						250					255	
cct	aga	gtt	tct	gtt	caa	aca	gct	tat	gga	gtg	gaa	gtt	gag	gtt	gat	818
Pro	Arg	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Asp	
				260					265					270		
aac	aat	cca	ttt	gac	ccg	agc	ctg	atg	gtt	ttc	atg	gat	tat	aga	gat	866
Asn	Asn	Pro	Phe	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	
			275					280					285			
tat	ctc	aga	cac	gac	gct	caa	tct	tta	gaa	gct	aaa	tat	cca	aca	ttt	914
Tyr	Leu	Arg	His	Asp	Ala	Gln	Ser	Leu	Glu	Ala	Lys	Tyr	Pro	Thr	Phe	
		290					295					300				
ctt	tat	gcc	atg	ccc	atg	tct	cca	aca	cga	gtc	ttt	ttc	gag	gaa	act	962
Leu	Tyr	Ala	Met	Pro	Met	Ser	Pro	Thr	Arg	Val	Phe	Phe	Glu	Glu	Thr	
		305				310					315					
tgt	ttg	gct	tca	aaa	gat	gca	atg	cca	ttc	gat	ctg	tta	aag	aaa	aaa	1010
Cys	Leu	Ala	Ser	Lys	Asp	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Lys	Lys	
320					325					330					335	
ctg	atg	cta	cga	ttg	aac	acc	ctt	ggt	gta	aga	att	aaa	gaa	att	tac	1058
Leu	Met	Leu	Arg	Leu	Asn	Thr	Leu	Gly	Val	Arg	Ile	Lys	Glu	Ile	Tyr	
				340					345					350		

gag gag gaa tgg tct tac ata ccg gtt ggt gga tct ttg cca aat aca 1106
 Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr
 355 360 365

gaa caa aaa aca ctt gca ttt ggt gct gct gct agc atg gtt cat cca 1154
 Glu Gln Lys Thr Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro
 370 375 380

gcc aca ggt tat tca gtc gtc aga tca ctt tct gaa gct cca aaa tgc 1202
 Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Cys
 385 390 395

gcc tct gta ctt gca aat ata tta cga caa cat tat agc aag aac atg 1250
 Ala Ser Val Leu Ala Asn Ile Leu Arg Gln His Tyr Ser Lys Asn Met
 400 405 410 415

ctt acc agt tca agt atc ccg agt ata tca act caa gct tgg aac act 1298
 Leu Thr Ser Ser Ser Ile Pro Ser Ile Ser Thr Gln Ala Trp Asn Thr
 420 425 430

ctt tgg cca caa gaa cga aaa cga caa aga tcg ttt ttc cta ttt gga 1346
 Leu Trp Pro Gln Glu Arg Lys Arg Gln Arg Ser Phe Phe Leu Phe Gly
 435 440 445

ctg gct ctg ata ttg cag ctg gat att gag ggg ata agg tca ttt ttc 1394
 Leu Ala Leu Ile Leu Gln Leu Asp Ile Glu Gly Ile Arg Ser Phe Phe
 450 455 460

cgc gca ttc ttc cgt gtg cca aaa tgg atg tgg cag gga ttt ctt ggt 1442
 Arg Ala Phe Phe Arg Val Pro Lys Trp Met Trp Gln Gly Phe Leu Gly
 465 470 475

tca agt ctt tct tca gca gac ctc atg tta ttt gcc ttc tac atg ttt 1490
 Ser Ser Leu Ser Ser Ala Asp Leu Met Leu Phe Ala Phe Tyr Met Phe
 480 485 490 495

att att gca cca aat gac atg aga aaa ggc ttg atc aga cat ctt tta 1538
 Ile Ile Ala Pro Asn Asp Met Arg Lys Gly Leu Ile Arg His Leu Leu
 500 505 510

tct gat cct act ggt gca aca ttg ata aga act tat ctt aca ttt 1583
 Ser Asp Pro Thr Gly Ala Thr Leu Ile Arg Thr Tyr Leu Thr Phe
 515 520 525

tagagtaaac tcctcctaca ataattgttg aatcagaggc ctcattactt cagattcata 1643
 acagaaatcg cggctctctcg aggcattgta tataacattt tcactagctt aata 1697

<210> 46
 <211> 526
 <212> PRT
 <213> *Lycopersicon esculentum*
 <400> 46

Met Glu Cys Val Gly Val Gln Asn Val Gly Ala Met Ala Val Leu Thr
 1 5 10 15

Arg Pro Arg Leu Asn Arg Trp Ser Gly Gly Glu Leu Cys Gln Glu Lys
 20 25 30

Ser Ile Phe Leu Ala Tyr Glu Gln Tyr Glu Ser Lys Cys Asn Ser Ser
 35 40 45

Ser Gly Ser Asp Ser Cys Val Val Asp Lys Glu Asp Phe Ala Asp Glu
 50 55 60

Glu Asp Tyr Ile Lys Ala Gly Gly Ser Gln Leu Val Phe Val Gln Met
 65 70 75 80

Gln	Gln	Lys	Lys	Asp	Met	Asp	Gln	Gln	Ser	Lys	Leu	Ser	Asp	Glu	Leu			
				85					90					95				
Arg	Gln	Ile	Ser	Ala	Gly	Gln	Thr	Val	Leu	Asp	Leu	Val	Val	Ile	Gly			
			100					105					110					
Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	Glu	Ser	Ala	Lys	Leu	Gly			
		115					120					125						
Leu	Asn	Val	Gly	Leu	Val	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	Tyr			
	130					135					140							
Gly	Val	Trp	Glu	Asp	Glu	Phe	Lys	Asp	Leu	Gly	Leu	Gln	Ala	Cys	Ile			
145					150					155					160			
Glu	His	Val	Trp	Arg	Asp	Thr	Ile	Val	Tyr	Leu	Asp	Asp	Asp	Glu	Pro			
				165					170					175				
Ile	Leu	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	His	Phe	Leu	His			
			180					185					190					
Glu	Glu	Leu	Leu	Lys	Arg	Cys	Val	Glu	Ala	Gly	Val	Leu	Tyr	Leu	Asn			
		195					200					205						
Ser	Lys	Val	Asp	Arg	Ile	Val	Glu	Ala	Thr	Asn	Gly	Gln	Ser	Leu	Val			
	210					215					220							
Glu	Cys	Glu	Gly	Asp	Val	Val	Ile	Pro	Cys	Arg	Phe	Val	Thr	Val	Ala			
225					230					235					240			
Ser	Gly	Ala	Ala	Ser	Gly	Lys	Phe	Leu	Gln	Tyr	Glu	Leu	Gly	Ser	Pro			
				245				250					255					
Arg	Val	Ser	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Asp	Asn			
			260					265					270					
Asn	Pro	Phe	Asp	Pro	Ser	Leu	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Tyr			
		275					280					285						
Leu	Arg	His	Asp	Ala	Gln	Ser	Leu	Glu	Ala	Lys	Tyr	Pro	Thr	Phe	Leu			
	290					295					300							
Tyr	Ala	Met	Pro	Met	Ser	Pro	Thr	Arg	Val	Phe	Phe	Glu	Glu	Thr	Cys			
305					310					315					320			
Leu	Ala	Ser	Lys	Asp	Ala	Met	Pro	Phe	Asp	Leu	Leu	Lys	Lys	Lys	Leu			
				325					330					335				
Met	Leu	Arg	Leu	Asn	Thr	Leu	Gly	Val	Arg	Ile	Lys	Glu	Ile	Tyr	Glu			
			340					345					350					
Glu	Glu	Trp	Ser	Tyr	Ile	Pro	Val	Gly	Gly	Ser	Leu	Pro	Asn	Thr	Glu			
		355				360						365						
Gln	Lys	Thr	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala			
	370					375					380							
Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys	Cys	Ala			
385					390					395					400			
Ser	Val	Leu	Ala	Asn	Ile	Leu	Arg	Gln	His	Tyr	Ser	Lys	Asn	Met	Leu			
				405					410					415				
Thr	Ser	Ser	Ser	Ile	Pro	Ser	Ile	Ser	Thr	Gln	Ala	Trp	Asn	Thr	Leu			
			420					425					430					
Trp	Pro	Gln	Glu	Arg	Lys	Arg	Gln	Arg	Ser	Phe	Phe	Leu	Phe	Gly	Leu			
		435					440					445						
Ala	Leu	Ile	Leu	Gln	Leu	Asp	Ile	Glu	Gly	Ile	Arg	Ser	Phe	Phe	Arg			
	450					455					460							

Ala	Phe	Phe	Arg	Val	Pro	Lys	Trp	Met	Trp	Gln	Gly	Phe	Leu	Gly	Ser
465					470					475					480
Ser	Leu	Ser	Ser	Ala	Asp	Leu	Met	Leu	Phe	Ala	Phe	Tyr	Met	Phe	Ile
				485					490					495	
Ile	Ala	Pro	Asn	Asp	Met	Arg	Lys	Gly	Leu	Ile	Arg	His	Leu	Leu	Ser
			500					505					510		
Asp	Pro	Thr	Gly	Ala	Thr	Leu	Ile	Arg	Thr	Tyr	Leu	Thr	Phe		
		515					520					525			

<210> 47
 <211> 510
 <212> DNA
 <213> Tagetes erecta
 <220>
 <221> misc_feature
 <222> (1)..(510)
 <223> coding for epsilon-cyclase specific probe

<400> 47
 ggcacgaggc aaagcaaagg ttgtttgttg ttgttgttga gagacactcc aatccaaaca 60
 gatacaaggc gtgactggat atttctctct cgttcctaac aacagcaacg aagaagaaaa 120
 agaatcatta ctaacaatca atgagtatga gagctggaca catgacggca acaatggcgg 180
 cttttacatg ccttaggttt atgactagca tcagatacac gaagcaaatt aagtgaacg 240
 ctgctaaaag ccagctagtc gttaaacaag agattgagga ggaagaagat tatgtgaaag 300
 ccggtggatc ggagctgctt ttgtttcaaa tgcaacagaa taagtccatg gatgcacagt 360
 ctagcctatc ccaaaagctc ccaagggtac caataggagg aggaggagac agtaactgta 420
 tactggattt ggttgtaatt ggttggtggtc ctgctggcct tgctcttgct ggagaatcag 480
 ccaagctagg cttgaatgtc gcacttatcg 510

<210> 48
 <211> 20
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 48
 ggcacgaggc aaagcaaagg 20

<210> 49
 <211> 21
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 49
 cgataagtgc gacattcaag c 21

<210> 50
 <211> 734
 <212> DNA
 <213> Tagetes erecta
 <220>
 <221> misc_feature

<222> (1)..(734)

<223> fragment of epsilon cyclase gene obtain by iPCR
comprising part of promoter region

<400> 50

```

ctaacaatca atgagtagag agctggacac atgacggcaa caatggcggc ttttacatgc 60
cctaggttta tgactagcat cagatacacg aagcaaatta agtgcaacgc tgctaaaagc 120
cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cgggtggatcg 180
gagctgcttt ttgttcaaat gcaacagaat aagtccatgg atgcacagtc tagcctatcc 240
caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat 300
gatattttaga tagattagct atcacctgtg ctgtggtgtg cagctcccaa gggctcttacc 360
gatagtaaaa tcgttagtta tgattaatac ttgggagggtg ggggattata ggctttgttg 420
tgagaatggt gagaaagagg tttgacaaat cgggtgtttga atgaggttaa atggagttaa 480
attaaaataa agagaagaga aagattaaga ggggtgatggg gatattaaag acggscaata 540
tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct 600
tggctgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta 660
ttgaatgcaa agcaaagcaa aggttgtttg ttgttgttgt tgagagacac tccaatccaa 720
acagatacaa ggcg                                     734

```

<210> 51

<211> 280

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(280)

<223> fragment of epsilon cyclase gene obtain by
TAIL-PCR comprising part of promoter region

<400> 51

```

gtcagtagtg gagttcaatt aaaataaaga gaagaraaag attaagaggg tgatggggat 60
attaaagacg gccaatrtag tgatgccacg taagaaaaag gtaagtgaaa acatacaacg 120
tggctttaaag agatggcttg gctgctaata aactcaactc aactcatatc ctatccattc 180
aaattcaatt caattctatt gaatgcaaag caaagcaaag caaaggttgt ttgttgttgt 240
tgttgagaga cactccaatc caaacagata caaggcgtga 280

```

<210> 52

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 52

```

cgccttgat ctgtttggat tgg                                     23

```

<210> 53

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 53

```

ctaacaatca atgagtatga gagc                                     24

```

<210> 54

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 54

agagcaaggc cagcaggacc acaacc

26

<210> 55

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 55

ccttgggagc ttttgggata ggctag

26

<210> 56

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 56

tcacgccttg tatctgttg gattgg

26

<210> 57

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 57

gtcgagtatg gagtt

15

<210> 58

<211> 734

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(734)

<223> coding for epsilon-cyclase genomic iPCR-fragment

<400> 58

ctaacaatca atgagtagag agctggacac atgacggcaa caatggcggc ttttacatgc	60
cctaggttta tgactagcat cagatacacg aagcaaatta agtgcaacgc tgctaaaagc	120
cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cggtaggatcg	180
gagctgcttt ttgttcaaat gcaacagaat aagtccatgg atgcacagtc tagcctatcc	240
caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat	300
gatatttaga tagattagct atcacctgtg ctgtggtgtg cagctcccaa gggctttacc	360
gatatgtaaaa tcgttagtta tgattaatac ttgggagggtg ggggattata ggctttgttg	420
tgagaatggt gagaaagagg tttgacaaat cgggtgtttga atgaggttaa atggagttta	480
attaaaataa agagaagaga aagattaaga gggtagatggg gatattaaag acggscaata	540
tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct	600
tggctgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta	660

ttgaatgcaa agcaaagcaa aggttgtttg ttgttgttgt tgagagacac tccaatccaa 720
acagatacaa ggcg 734

<210> 59

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 59

ctcgagagta aaatcgtttag ttatg 25

<210> 60

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 60

ccatggccat tgattgtag taatgattc 29

<210> 61

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 61

ccatggtaat ttgcttcgtg tatctgatg 29

<210> 62

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 62

ccatggcgct agcagcgaca gtaatg 26

<210> 63

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 63

gatatccggt gtgagggaac tag 23

<210> 64

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 64

gcaagctcga cagctacaaa cc

22

<210> 65

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
oligonucleotide primer

<400> 65

gaagcatgca gctagcagcg acag

24

<210> 66

<211> 1795

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: coding for
ketolase - 35S terminator construct

<400> 66

```

ccatggcgct agcagcgaca gtaatgttgg agcagcttac cggaagcgct gaggcactca 60
aggagaagga gaaggaggtt gcaggcagct ctgacgtgtt gcgtacatgg gcgacccagt 120
actcgcttcc gtcagaggag tcagacgcgg cccgcccggg actgaagaat gcctacaagc 180
caccaccttc cgacacaaaag ggcatacaca tggcgctagc tgtcatcggc tcctggggccg 240
cagtgttcct ccacgccatt tttcaaatca agcttccgac ctcttggac cagctgcact 300
ggctgcccgt gtcagatgcc acagctcagc tggttagcgg cagcagcagc ctgctgcaca 360
tcgtcgtagt attctttgtc ctggagttcc tgtacacagg cctttttatc accacgcatg 420
atgctatgca tggcaccatc gccatgagaa acaggcagct taatgacttc ttgggcagag 480
tatgcatctc cttgtacgcc tggtttgatt acaacatgct gcaccgcaag cattggggagc 540
accacaacca cactggcgag gtgggcaagg accctgactt ccacagggga aaccctggca 600
ttgtgccctg gtttgccagc ttcattgtcca gctacatgtc gatgtggcag tttgcgcgcc 660
tcgcatggtg gacggtggtc atgcagctgc tgggtgcgcc aatggcgaac ctgctggtgt 720
tcatggcggc cgcgcccatt ctgtccgcct tccgcttgtt ctactttggc acgtacatgc 780
cccacaagcc tgagcctggc gccgcgtcag gctcttcacc agccgtcatg aactgggtgga 840
agtcgcgcac tagccaggcg tccgacctgg tcagctttct gacctgtac cacttcgacc 900
tgcactggga gcaccaccgc tggccctttg ccccttggtg ggagctgcc aactgccgcc 960
gcctgtcttg ccgaggtctg gttcctgcct agctggacac actgcagtgg gccctgctgc 1020
cagctgggca tgcctgcagg tcgacggatc cccgggaatt cggtagctg aaatcaccag 1080
tctctctcta caaatctatc tctctctatt ttctccataa ataatgtgtg agtagtttcc 1140
cgataaggga aattagggtt cttatagggt ttcgtcatg tgttgagcat ataagaaacc 1200
cttagtatgt atttgtattt gtaaaatact tctatcaata aaatttctaa ttcctaaaac 1260
caaaatccag tactaaaatc cagatctcct aaagtcccta tagatctttg tcgtgaatat 1320
aaaccagaca cgagacgact aaacctggag cccagacgcc gttcgaagct agaagtaccg 1380
cttaggcagg agcccggttag ggaaaagatg ctaaggcagg gttgggttac ttgactcccc 1440
cgtaggtttg gtttaaatat gatgaagtgg acggaaggaa ggaggaagac aaggaaggat 1500
aaggttgcag gccctgtgca aggtaagaag atggaaattt gatagaggta cgctactata 1560
cttatactat acgctaaggg aatgcttgta tttataccct atacccccta ataaccctt 1620
atcaatttaa gaaataatcc gcataagccc ccgcttaaaa attggtatca gagccatgaa 1680
taggtctatg accaaaactc aagaggataa aacctcacca aaatacgaaa gagttcttaa 1740
ctctaaagat aaaagatctt tcaagatcaa aactagttcc ctcacaccgg atatac 1795

```

<210> 67

<211> 28

<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
oligonucleotide primer
<400> 67
gagctcactc actgatttcc attgcttg 28
<210> 68
<211> 37
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
oligonucleotide primer
<400> 68
cgccgttaag tcgatgtccg ttgatttaaa cagtgtc 37
<210> 69
<211> 34
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
oligonucleotide primer
<400> 69
atcaacggac atcgacttaa cggcgtttgt aaac 34
<210> 70
<211> 25
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
oligonucleotide primer
<400> 70
taagctttttt gttgaagaga tttgg 25
<210> 71
<211> 28
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
oligonucleotide primer
<400> 71
gtcgactacg taagtttctg cttctacc 28
<210> 72
<211> 26
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
oligonucleotide primer

<400> 72
 ggatccggtg atacctgcac atcaac 26
 <210> 73
 <211> 28
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer
 <400> 73
 aagcttaccg atagtaaaat cgtagtt 28
 <210> 74
 <211> 31
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer
 <400> 74
 ctcgagctta ccgatagtaa aatcgtagt t 31
 <210> 75
 <211> 28
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer
 <400> 75
 gtcgacaaca acaacaaaca acctttgc 28
 <210> 76
 <211> 28
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence:
 oligonucleotide primer
 <400> 76
 ggatccaaca acaacaaaca acctttgc 28
 <210> 77
 <211> 777
 <212> DNA
 <213> Arabidopsis thaliana
 <220>
 <221> promoter
 <222> (1)..(777)
 <223> modified version of the AP3 promoter
 <400> 77
 gagctcactc actgatttcc attgcttgaa aattgatgat gaactaagat caatccatgt 60
 tagtttcaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactggtcga 120
 agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagttagga 180
 ccaaacatta tctacaaaca aagacttttc tcctaacttg tgattccttc ttaaacccta 240

```

ggggtaatat tctattttcc aaggatcttt agttaaaggg aaatccggga aattattgta 300
atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360
tatatatctc tttcttctta tttcccaa ataacagacaa aagtagaata ttggctttta 420
acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgc 480
aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540
ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600
tcacttagtt ttcactcaact tctgaactta cttttcatgg attaggcaat actttccatt 660
tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcact 720
tctttcttct cattatatct cttgtcctct ccaccaaata tcttcaacaa aaagctt 777

```

<210> 78

<211> 212

<212> DNA

<213> Solanum tuberosum

<220>

<221> intron

<222> (1)..(212)

<223> PIV2 intron of ST-LS1 gene

<400> 78

```

gtcgactacg taagtttctg cttctacctt tgatatatat ataataatta tcattaatta 60
gtagtaatat aatatttcaa atattttttt caaaataaaa gaatgtagta tatagcaatt 120
gcttttctgt agtttataag tgtgtatatt ttaatttata acttttctaa tatatgacca 180
aaatttggtg atgtgcaggt atcaccggat cc 212

```

<210> 79

<211> 358

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(358)

<223> coding for sense-strand of epsilon cyclase
promoter directed dsRNA

<400> 79

```

aagcttaccg atagtaaaat cgtagttat gattaatact tgggaggtgg gggattatag 60
gctttgttgt gagaatggtg agaaagaggt ttgacaaatc ggtggttgaa tgaggttaaa 120
tgaggtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180
cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240
aagatggctt ggctgcta atcaactcaact caactcatat cctatccatt caaattcaat 300
tcaattctat tgaatgcaaa gcaaagcaaa gcaaagggtt tttgttggtt ttgtcgac 358

```

<210> 80

<211> 361

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(361)

<223> coding for antisense-strand of epsilon cyclase
promoter directed dsRNA

<400> 80

```

ctcgagctta ccgatatgaa aatcgttagt tatgattaat acttgggagg tgggggatta 60
taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgaggtt 120
aatggaggtt taattaaaaa aaagagaaga gaaagattaa gagggatgat gggatattaa 180
agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240
taaaagatgg cttggctgct aatcaactca actcaactca tatcctatcc attcaaattc 300
aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttggtt ttgttgatc 360
c 361

```

<210> 81
 <211> 1537
 <212> DNA
 <213> Cucumis sativus
 <220>
 <221> promoter
 <222> (1)..(1537)
 <223> promoter of chromoplast-specific
 carotenoid-associated protein (CHRC)

<400> 81
 gagctctaca aattaggggtt actttattca ttttcatcca ttctctttat tgttaaattt 60
 tgtacattta ttcaataata ttatatgttt attacaaatt ctacttttct tattcatacc 120
 tattcactca agcctttacc atcttccttt tctatttcaa tactatttct acttcatttt 180
 tcacgttttt aacatctttc tttatttctt gtccacttcg tttagggatg cctaattgtcc 240
 caaatttcat ctctcgtagt aacacaaaac caatgtaatg ctacttctct ctacattttt 300
 aatacaaata aagtgaacaa aaatatctat aaataaacia atatataat tttgttagac 360
 gctgtctcaa cccatcaatt aaaaaatttt gttatatttc tactttacct actaaatttg 420
 tttctcatat ttacctttta acccccacaa aaaaaaatta taaaaaagaa agaaaaaagc 480
 taaaccctat ttaaatagct aactataaga tcttaaaatt atcctcatca gtgtatagtt 540
 taattgggta ttaacttata acattatata tctatgacat atactctctc ctacttattt 600
 ctcacatttt ttaacttaag aaaatagtca taacatagtc taaaattcaa acatccacat 660
 gctctaattt gattaacaaa aagttagaaa tattttattta aataaaaaaag actaataaat 720
 atataaaatg aatgttcata cgcagacca tttagagatg agtatgcttt cacatgctga 780
 gattattttc aaaactaagg ttgtagcaat attaaatcaa taaaattatt ataaataaca 840
 aaattaacct gctcgtgttt gctgtatatg ggaggctaca aaataaatta aactaaagat 900
 gattatgttt tagacatttt ttctatctgt attagtttat acatattaat tcaggagctg 960
 cacaacccaa ttctattttc gttccttggt ggctggggtt ctcacaaggt tcaatagtca 1020
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